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(54) Title: CELL LINES AND HOST NUCLEIC ACID SEQUENCES RELATED TO INFECTIOUS DISEASE

(57) Abstract: Host nucleic acids and host proteins that participate in viral infection, such as human immunodeficiency virus (HIV), influenza A, and Ebola virus, have been identified. Interfering with or disrupting the interaction between a host nucleic acid or host protein and a virus or viral protein confers an inhibition of or resistance to infection. Thus, interfering with such an interaction in a host subject can confer a therapeutic or prophylactic effect against a virus. The sequences identified can be used to identify agents that reduce or inhibit viral infection.

CELL LINES AND HOST NUCLEIC ACID SEQUENCES RELATED TO
INFECTIOUS DISEASE

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application Nos. 60/427,464 filed November 18, 2002 and 60/482,604 filed June 25, 2003, both herein incorporated by reference.

FIELD

The present disclosure relates to host nucleic acid sequences, and proteins encoded by these sequences, that are involved in viral infection or are otherwise associated with the life cycle of a virus. Decreasing or inhibiting the interaction of these host sequences with a viral sequence can be used to decrease or inhibit infection by the virus.

BACKGROUND

Infectious diseases affect the health of people and animals around the world, causing serious illness and death. Public health efforts have focused on behavioral modification and other public health efforts to reduce the incidences of infection, while treatment regimens for these diseases have focused on pharmaceuticals, such as antibiotics and anti-viral medications. However, educating people about modifying behavior can be difficult, and that approach alone rarely can significantly diminish the incidence of infection. Furthermore, modifying the behavior of domestic or wild animals would not result in diminished infections. Stopping the spread of infections in an animal population typically involves wholesale slaughter. Few vaccines are available or wholly effective, and they tend to be specific for particular conditions.

The rate of HIV (human immunodeficiency virus) infection is increasing. HIV and its associated acquired immune deficiency syndrome (AIDS) accounted for approximately 5% of all deaths in the United States in the year 2000, while over 313,000 persons were reported to be living with AIDS in that same year. Centers for Disease Control and Prevention, *HIV/AIDS Surveillance Supplemental Report*, 8(1):1-22 (2002). These increasing infection rates have occurred, even though the mode of HIV infection has been known for almost 20 years, and educational programs around the world have promoted behavioral modifications meant to reduce HIV infection. Incidence and death rates due to HIV disease have been decreasing since the mid-90's, in part due to aggressive antiviral therapies, which frequently have toxic side effects and strict dosage schedules. However, even with treatment, the patient is not cured of the disease, and to date, no effective vaccine therapy has been found.

In other diseases, such as infection by the Ebola virus, not only are treatments limited, but containment or prevention of infections is difficult because the life cycle of the virus is not well known. The natural reservoir for the Ebola virus, that is the place or population in nature where the virus resides between human outbreaks, has not yet been identified.

2

Additionally, different viral strains can rapidly evolve in response to drug usage, producing drug-resistant strains. For example, strains of the influenza virus resistant to amantadine and rimantadine have recently arisen. A recent study of 80 newly-infected people conducted by the AIDS Research Center at Rockefeller University in New York, found that as many as 16.3% of these individuals had strains of HIV associated with resistance to some treatments, and 3.8% appeared to be resistant to several currently available anti-HIV drugs. Thus, a need exists for alternative treatments for infectious disease and methods of designing new drugs to combat infectious disease.

SUMMARY

Several host nucleic acid sequences involved in viral infection have been identified using gene trap methods. The identification of these host sequences and their encoded products permits the identification of sequences that can be targeted for therapeutic intervention.

The disclosed host sequences (including the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, and the proteins encoded thereby (such as SEQ ID NOS: 228, 230, and 232), as well as variants, fusions, and fragments thereof that retain the appropriate biological activity) can mediate infection, and in some examples these host nucleic acids are required for infection. For example, the host nucleic acid can encode a cellular receptor or ligand or a fragment thereof that is recognized by a virus, such as the T-cell V-D-J beta 2.1 chain. In another example, the host nucleic acid encodes an enzyme that mediates viral infection, such as the β-chimerin rho-GTPase (referred to herein as β-chimerin). In another example, the host nucleic acid encodes a Ras oncogene family member such as Rab9. It is demonstrated herein that Rab9 is a host protein involved in infection by pathogens (such as viruses and bacteria) that use similar pathways for morphogenesis of infectious particles. In particular examples, Rab9 is involved in infection by pathogens (such as viruses and bacteria) that utilize lipid rafts. Thus, for example, interfering with the interaction between the disclosed host proteins and a viral or pathogen protein, for example by disrupting the expression of the host nucleic acid within a host cell, or by administering an agent that decreases binding between a host protein and a viral protein, can inhibit, or even prevent, infection of that host cell by the associated virus. Moreover, the identification of particular host enzymes or other host proteins involved in infection provides a method for developing new therapies targeted at inhibiting infection, at the protein or nucleic acid level.

In some examples, the nucleic acid itself mediates viral infection. For example, the nucleotide sequence of a host nucleic acid in the host genome can be recognized by the virus during integration of the viral genome into the host genome. The identification of nucleic acid sequences that are involved in the pathogenesis of infection therefore provides an important tool for interfering with infection.

This genomics-based discovery of nucleic acids and proteins involved in, or even required for, infection provides a new paradigm for identifying and validating various aspects of infectious disease, including assessing individual or population resistance to infection and finding novel

diagnostic and drug targets for infectious disease and altering the nucleotide sequence of the host nucleic acid.

Based on the identification of several host nucleic acid and protein sequences involved in viral infection, provided herein are methods for decreasing infection of a host cell by a virus, such as HIV, Ebola, or influenza A, or treating such a viral infection, by interfering with the activity or expression of one or more host proteins shown in Table 1 (including the target sequences associated with any of SEQ ID NOS: SEQ ID NOS: 1-232, as well as variants, fragments, and fusions thereof), such as at least two host proteins, or at least three host proteins. Also provided are methods for identifying agents that can decrease viral infection of a host cell, such as infection by HIV, Ebola, or influenza A. In addition, cells and non-human mammals are provided that have decreased susceptibility to viral infection, such as HIV, Ebola, or influenza A infection.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is a schematic illustration of the U3neoSV1 retroviral vector, which is capable of isolating the nucleic acids described herein using the gene-trap method.

FIG. 2 is a schematic illustration of the gene-trap method.

FIG. 3 is a schematic illustration of one method of identifying host genes described herein.

FIG. 4 is a flow chart illustrating a method for isolating cells resistant to HIV infection, including HIV-1 and HIV-2 infection.

FIG. 5 is a bar graph showing the relative amount of p24 in HIV-infected cells in the presence of various siRNAs. CHN (β-chimerin); KOX (similar to KOX4 (LOC131880) and LOC166140); RBB (retinoblastoma binding protein 1); RAB (Rab9); KIAA1259; F3 (tissue factor 3; thromboplastin); AXL (AXL receptor tyrosine kinase); Msleb (mammalian selenium binding protein).

FIG. 6 is a schematic drawing showing a model of Rab9 involvement in lipid raft formation.

SEQUENCE LISTING

The nucleotide sequences of the nucleic acids described herein are shown using standard letter abbreviations for nucleotide bases, and three letter code for amino acids. Only one strand of each nucleic acid sequence is shown, but the complementary strand is understood as included by any reference to the displayed strand. Additionally, the nucleic acid sequences shown in SEQ ID NOS: 1-226 inherently disclose the corresponding polypeptide sequences of coding sequences (resulting translations of the nucleotide sequences), even when those polypeptide sequences are not explicitly provided herein.

SEQ ID NO: 1 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E8, entire insert. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor V beta chain (T-cell receptor beta). Further information on the T-cell receptor V beta chain can be found in WO 01/23409, WO 01/55302, WO 01/57182, and WO 01/94629.

4

SEQ ID NO: 2 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BA, distal end. The human homolog is the (-) strand of GenBank Accession No. AC104597.3, T-cell receptor V beta chain.

SEQ ID NO: 3 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BA, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 4 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, distal end. The human homolog is the (+) strand of GenBank Accession No. AC00616.7, T-cell receptor beta.

SEQ ID NO: 5 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, middle of insert. The human homolog is the (-) strand of GenBank Accession No. AC104597.3, T-cell receptor beta.

SEQ ID NO: 6 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BE, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 7 is a nucleic acid sequence associated with viral, such as HIV, infection which corresponds to the sequence identified as Nucleotide Sequence 18E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 8 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E21, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 9 is a nucleic acid sequence associated with viral, such as HIV, infection which corresponds to the sequence identified as Nucleotide Sequence 2E22, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC099395.2, T-cell receptor beta.

SEQ ID NO: 10 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B13, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 11 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B14, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 12 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B15, distal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 13 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B15, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 14 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B16, proximal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

5

SEQ ID NO: 15 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E23, distal end. The human homolog is the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 16 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E23, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 17 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E24, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 18 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E25, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 19 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E26, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 20 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18BD, proximal end. The human homolog is the (+) strand of GenBank Accession No. M16834.1, T-cell receptor V-D-J-beta 2.1 chain (described in WO 02/057414 and Reynolds *et al.*, *Cell* 50(1):107-17, 1987).

SEQ ID NO: 21 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E7, distal end. The human homolog is the (-) strand of GenBank Accession No. AC004593.1 including beta-chimaerin rho GTPase (CHN2) (for example see WO 01/12659).

SEQ ID NO: 22 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 18E7, proximal end. The human homologs are the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta; and the (+) strand of GenBank Accession No. AC004593.1 including beta-chimaerin (CHN2).

SEQ ID NO: 23 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AL049699.8, including malic enzyme 1 (ME1) NADP(+)-dependent cytosolic. Further information on this gene can be found in WO 01/55301 and WO 01/53312.

SEQ ID NO: 24 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18BD, distal end. The human homolog is the (+) strand of GenBank Accession No. AC123903.1, including hypothetical protein XP_174419.

SEQ ID NO: 25 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, distal end. The human

6

homolog is the (+) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 26 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, middle of insert. The human homolog is the (+) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.

SEQ ID NO: 27 is a nucleic acid sequence associated with viral, such as HIV and influenza A, infection, and is the clone identified as Nucleotide Sequence 18E9, proximal end. The human homologs are the (-) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta; and (-) strand of GenBank Accession No. AC096736.3, a region of chromosome 4q31.3-32.'

SEQ ID NO: 28 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E21, distal end. The human homolog is the (-) strand of GenBank Accession No. M26920.1, alpha satellite DNA.

SEQ ID NO: 29 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E22, distal end. The human homologs are the (+) strand of GenBank Accession No. AP004369.3, including LOC253788 (and neighboring similar to RIKEN cDNA 1700001L23 (LOC219938)); and the (+) strand of GenBank Accession No. AC093117.2, between coagulation factor III, thromboplastin, tissue factor (F3) and LOC91759.

SEQ ID NO: 30 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B13, distal end. The human homolog is the (-) strand of GenBank Accession No. AC092043.2, between similar to zinc finger protein 7 KOX4 (LOC131880) and LOC166140.

SEQ ID NO: 31 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B14, distal end. The human homologs are the (-) strand of GenBank Accession No. AL136963.17, between LOC222474 and similar to Rho guanine nucleotide exchange factor 4, isoform a, APC-stimulated guanine nucleotide exchange factor (LOC221178); and the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 32 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2B16, distal end. The human homolog is the (-) strand of GenBank Accession No. AL133293.28, between ribosomal protein L7A-like 4 (RPL7AL4) and v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC).

SEQ ID NO: 33 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E24, distal end. The human homolog is the (-) strand of GenBank Accession No. AL161417.17, KIAA0564.

SEQ ID NO: 34 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E25, distal end. The human homologs are the (-) strand of GenBank Accession No. Z12006.1, alpha satellite DNA; and the (+) and (-) strands of GenBank Accession No. AC093577.2, M96 protein.

SEQ ID NO: 35 is a nucleic acid sequence associated with viral, such as HIV, infection, and is the clone identified as Nucleotide Sequence 2E26, distal end. The human homologs are the (-) strand of GenBank Accession No. Z78022.1, hypothetical protein similar to G proteins, especially RAP-2A (LOC57826); and the (+) strand of GenBank Accession No. AL136220.14, between LOC161005 and osteoblast specific factor 2 (fasciclin I-like; OSF-2).

SEQ ID NO: 36 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3B1, distal end. The canine homolog is the (+) and (-) strand portions of GenBank Accession No. AJ012166.1, *Canis familiaris* TCTA gene, AMT gene, DAG1 gene, and BSN gene.

SEQ ID NO: 37 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5B5, distal end. The canine homolog is the (+) and (-) strand portions of GenBank Accession No. AJ012166.1, *Canis familiaris* TCTA gene, AMT gene, DAG1 gene, and BSN gene.

SEQ ID NO: 38 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 39 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B2, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 40 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 41 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 42 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1B6, distal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 43 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E3, entire insert. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 44 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E5, proximal end. The human

8

homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 45 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6B1, entire insert. The human

5   homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 46 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC117507.5, including LIM domain containing

10   preferred translocation partner in lipoma (LPP).

SEQ ID NO: 47 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

15   SEQ ID NO: 48 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC117507.5, including LIM domain containing preferred translocation partner in lipoma (LPP).

SEQ ID NO: 49 is a nucleic acid sequence associated with viral, such as influenza A,

20   infection, and is the clone identified as Nucleotide Sequence B1E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC104036.8, between LOC253121 and hyaluronan synthase 2 (HAS2).

SEQ ID NO: 50 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E1, proximal end. The human

25   homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3 (see WO 01/57270, WO 01/57271, WO 01/57273, WO 01/57274, WO 01/57275, WO 01/57276, WO 01/57277, WO 01/57278, or Tatarelli *et al.*, *Genomics* 68(1):1-12, 2000).

SEQ ID NO: 51 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E4, distal end. The human homolog

30   is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 52 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B1E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 53 is a nucleic acid sequence associated with viral, such as influenza A,

35   infection, and is the clone identified as Nucleotide Sequence B6E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 54 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 55 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 56 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B7E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 57 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B7E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and Testin 3.

SEQ ID NO: 58 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL133230.25, PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1 (see Watanabe *et al.*, *Jpn. J. Cancer Res.* 93:1114-22, 2002).

SEQ ID NO: 59 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B5E2, middle of insert. The human homolog is the (-) strand of GenBank Accession No. AL133230.25, PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1.

SEQ ID NO: 60 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3E11, distal end. The human homolog is the (+) strand of GenBank Accession No. AL445675.9, between LOC149360 and LOC253961.

SEQ ID NO: 61 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B3E11, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL391986.12, between KIAA1560 and Tectorin beta (TECTB).

SEQ ID NO: 62 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AC016826.9, including Cadherin related 23 (CDH23).

SEQ ID NO: 63 is a nucleic acid sequence associated with viral, such as influenza A, infection, and is the clone identified as Nucleotide Sequence B6E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AL357372.12, Myeloid/lymphoma or mixed lineage leukemia, translocated to 10 (MMLT10).

SEQ ID NO: 64 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AL355802.13, between exportin 5 (XPO5) and DNA polymerase eta (POLH).

SEQ ID NO: 65 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1B5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL355802.13, between XPO5 and POLH.

SEQ ID NO: 66 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence ZV1-1E, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL355802.13, between XPO5 and POLH.

SEQ ID NO: 67 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including heterogenous nuclear riboprotein C (C1/C2) (HNRPC).

SEQ ID NO: 68 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 69 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 70 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 71 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B13, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 72 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B14, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 73 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B21, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 74 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B25, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 75 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B35, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL135744.4, including HNRPC.

SEQ ID NO: 76 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E5, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AL050324.5, including alpha-endosulfine pseudogene (ENSAP) and LOC128741.

SEQ ID NO: 77 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AC017060.7, including LOC222888.

11

SEQ ID NO: 78 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B13, distal end. The human homolog is the (+) strand of GenBank Accession No. AL161731.20, between LOC138421 and zinc finger protein 297B (ZNF297B).

5   SEQ ID NO: 79 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B14, distal end. The human homolog is the (-) strand of GenBank Accession No. AC012366.10, including sideroflexin 5 (SFXN5).

SEQ ID NO: 80 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV1-2B35, distal end. The human homolog is the 10   (+) strand of GenBank Accession No. AL645504.10, including importin 9 (FLJ10402).

SEQ ID NO: 81 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence GV1-1B1, distal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 82 is a nucleic acid sequence associated with viral, such as Ebola, infection, 15   and is the clone identified as Nucleotide Sequence GV1-1B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. NG_001333.1, T-cell receptor beta.

SEQ ID NO: 83 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

20   SEQ ID NO: 84 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 85 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E2, proximal end. The human homolog is 25   the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 86 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 87 is a nucleic acid sequence associated with viral, such as Ebola, infection, 30   and is the clone identified as Nucleotide Sequence MV2-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 88 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

35   SEQ ID NO: 89 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 90 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 91 is a nucleic acid sequence associated with viral, such as Ebola, infection,
5 and is the clone identified as Nucleotide Sequence MV3-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 92 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

10 SEQ ID NO: 93 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 94 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-B1, distal end. The human homolog is the
15 (+) and (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 95 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 96 is a nucleic acid sequence associated with viral, such as Ebola, infection,
20 and is the clone identified as Nucleotide Sequence MV6-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 97 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

25 SEQ ID NO: 98 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 99 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E5, proximal end. The human homolog is
30 the (-) strand of GenBank Accession No. AC058791.4, adjacent to LOC135952.

SEQ ID NO: 100 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC021753.7, hypothetical protein KIAA1259.

SEQ ID NO: 101 is a nucleic acid sequence associated with viral, such as Ebola, infection,
35 and is the clone identified as Nucleotide Sequence MV2-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC021753.7, hypothetical protein KIAA1259.

SEQ ID NO: 102 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E3, distal end. The human homolog is the

(+) and (-) strands of GenBank Accession No. AC107081.5, copper metabolism gene (MURR1) and chaperonin containing TCP1, subunit 4 (CCT4).

SEQ ID NO: 103 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC099785.2, hypothetical protein FLJ40773 and similar to ribosomal protein L24-like (LOC149360).

SEQ ID NO: 104 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 105 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV2-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 106 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 107 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AF260225.1, Testin 2 and 3 (TES).

SEQ ID NO: 108 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B2, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC105934.2, polybromo 1 (PB1).

SEQ ID NO: 109 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B4, distal end. The human homolog is the (+) strand of GenBank Accession No. AC022506.38, between DNA damage inducible transcript 3 (DDIT3) and KIAA1887.

SEQ ID NO: 110 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-B5, distal end. The human homolog is the (-) strand of GenBank Accession No. AL157834.12, PDZ and LIM domain 1 (elfin) (PDLIM1).

SEQ ID NO: 111 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AL110115.38, LOC284803.

SEQ ID NO: 112 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL110115.38, signal peptide peptidase (HM13) and LOC284803.

SEQ ID NO: 113 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL117341.26, containing PRO0097 and adjacent to FLJ31958.

SEQ ID NO: 114 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AP002076.3, small inducible cytokine E, member 1 (endothelial monocyte-activating) (SCYE1).

SEQ ID NO: 115 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AP002076.3, containing SCYE1.

SEQ ID NO: 116 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. AP002076.3, containing SCYE1.

SEQ ID NO: 117 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E4, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC132812.9, between E3 ubiquitin ligase (SMURF2) and hypothetical protein MGC40489.

SEQ ID NO: 118 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC079383.17, Ras oncogene family member Rab9.

SEQ ID NO: 119 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV3-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC079383.17, Ras oncogene family member Rab9.

SEQ ID NO: 120 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL132989.5, between PRO1617 and retinoblastoma binding protein 1 (RBBP1).

SEQ ID NO: 121 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL132989.5, RBBP1.

SEQ ID NO: 122 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL132989.5, retinoblastoma binding protein 1 (RBBP1).

SEQ ID NO: 123 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E3, distal end. The human homolog is the (+) and (-) strands of GenBank Accession No. AC096669.1, a region of chromosome 2q12.

SEQ ID NO: 124 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV6-E4, distal end. The human homolog is the (-) strands of GenBank Accession No. AF196968.4, elongation factor for selenoprotein translation (SELB).

15

SEQ ID NO: 125 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-B1, distal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 126 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 127 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 128 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 129 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 130 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 131 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E4, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 132 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 133 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E6, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 134 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E7, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 135 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E8, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 136 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E9, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

SEQ ID NO: 137 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E10, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC112218.2, transcription factor SMIF (HSA275986).

16

SEQ ID NO: 138 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AL031293.1, KIAA1026.

SEQ ID NO: 139 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E3, distal end. The human homolog is the (+) strand of GenBank Accession No. AL035587.5, trinucleotide repeat containing 5 (TNRC5).

SEQ ID NO: 140 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC126182.2, homogentisate 1,2-dioxygenase (HGD).

SEQ ID NO: 141 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AL591643.4, a region of chromosome Xq23-24.

SEQ ID NO: 142 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E6, distal end. The human homolog is the (-) strand of GenBank Accession No. AC113603.3, a region of chromosome 4p15.3.

SEQ ID NO: 143 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC011995.8, similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883).

SEQ ID NO: 144 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E8, distal end. The human homolog is the (-) strand of GenBank Accession No. AC084208.5, a region of chromosome 2q21.

SEQ ID NO: 145 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL391259.15, a region of chromosome Xp11.4, including ubiquitin specific protease 9 (USP9X).

SEQ ID NO: 146 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV13-E10, distal end. The human homolog is the (+) strand of GenBank Accession No. AC006397.1, LOC221829.

SEQ ID NO: 147 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B2, distal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 148 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B2, proximal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 149 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 150 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 151 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 152 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 153 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV8-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 154 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV8-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. X14945.1, U3 small nuclear RNA gene.

SEQ ID NO: 155 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B3, distal end. The human homolog is the (+) strand of GenBank Accession No. AL365203.19, integrin, beta 1 (ITGB1).

SEQ ID NO: 156 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-B3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AL365203.19, ITGB1.

SEQ ID NO: 157 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL365203.19, ITGB1.

SEQ ID NO: 158 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL365203.19, ITGB1.

SEQ ID NO: 159 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AP001132.4, acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1).

SEQ ID NO: 160 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV7-E5, distal end. The human homolog is the (-) strand of GenBank Accession No. AK025453.1, prospero-related homeobox 1 (PROX1).

SEQ ID NO: 161 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

18

SEQ ID NO: 162 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 163 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E3, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 164 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E4, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 165 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 166 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 167 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E8, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 168 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E9, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 169 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E9, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 170 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E10, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 171 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E10, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 172 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ20627.

SEQ ID NO: 173 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, between hypothetical proteins FLJ20627 and FLJ12910.

SEQ ID NO: 174 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC105001.3, between PIN2-interacting protein 1 (PINX1) and SRY (sex-determining region Y)-box7 (SOX7).

SEQ ID NO: 175 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E2, distal end. The human homolog is the (-) strand of GenBank Accession No. AC009520.16, LOC131920.

SEQ ID NO: 176 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E3, distal end. The human homolog is the (-) strand of GenBank Accession No. AL596329.5, a region of chromosome 13q14.

SEQ ID NO: 177 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E5, distal end. The human homolog is the (+) strand of GenBank Accession No. AC023844.6, neurotrophic tyrosine kinase, receptor, type 3 (NTRK3).

SEQ ID NO: 178 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E7, promimal end. The human homolog is the (-) strand of GenBank Accession No. AC024940.39, between TERA protein (TERA) and hypothetical protein FLJ13224.

SEQ ID NO: 179 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC024940.39, flanking TERA protein (TERA) and hypothetical protein FLJ13224.

SEQ ID NO: 180 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E8, distal end. The human homolog is the (-) strand of GenBank Accession No. AC084335.6, hypothetical gene LOC284260.

SEQ ID NO: 181 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E11, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC073108.9, POM (POM121 homolog) and ZP3 fusion (POMZP3).

SEQ ID NO: 182 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV14-E11, distal end. The human homolog is the (-) strand of GenBank Accession No. AC073108.9, POM (POM121 homolog) and ZP3 fusion (POMZP3).

SEQ ID NO: 183 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV19-E4, distal end. The human homolog is the (+) strand of GenBank Accession No. AC087650.12, between DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064).

SEQ ID NO: 184 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E2, distal end. The human homolog is the

(-) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 185 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E2, proximal end. The human homolog is

5   the (+) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 186 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-B1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC105285.3, LOC345307 and UDP-N-acetyl-D-

10   galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7).

SEQ ID NO: 187 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E3, distal end. The murine homolog is the (+) strand of GenBank Accession No. NG_001440.1, *Mus musculus* 5S rRNA pseudogene (Rn5s-ps1).

15   SEQ ID NO: 188 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E5, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2).

SEQ ID NO: 189 is a nucleic acid sequence associated with viral, such as Ebola, infection,

20   and is the clone identified as Nucleotide Sequence MV28-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 190 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

25   SEQ ID NO: 191 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E9, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 192 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E9, distal end. The human homolog is the

30   (-) strand of GenBank Accession No. AL121886.22, between RPL27AP and MYBL2.

SEQ ID NO: 193 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E6, distal end. The human homolog is the (+) strand of GenBank Accession No. AP000711.4, Down's syndrome cell adhesion molecule like 1 (DSCAML1).

35   SEQ ID NO: 194 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AL391555.19, LOC148529.

SEQ ID NO: 195 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV20-B4, distal end. The human homolog is the

21

(-) strand of GenBank Accession No. AC112129.4, Huntingtin-associated protein interacting protein (HAPIP).

SEQ ID NO: 196 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E1, proximal end. The human homolog is
5   the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 197 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN
10   cDNA 1210001E11 (LOC347366).

SEQ ID NO: 198 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

15   SEQ ID NO: 199 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E5, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 200 is a nucleic acid sequence associated with viral, such as Ebola, infection,
20   and is the clone identified as Nucleotide Sequence MV22-E8, proximal end. The human homolog is the (-) strand of GenBank Accession No. Z69732.1, between LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366).

SEQ ID NO: 201 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E2, distal end. The human homolog is the
25   (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 202 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E2, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 203 is a nucleic acid sequence associated with viral, such as Ebola, infection,
30   and is the clone identified as Nucleotide Sequence MV22-E6, distal end. The human homolog is the (-) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

SEQ ID NO: 204 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E6, proximal end. The human homolog is the (+) strand of GenBank Accession No. AL590543.8, hypothetical protein FLJ12910.

35   SEQ ID NO: 205 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AC005284.1, LOC350411.

SEQ ID NO: 206 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV22-E9, proximal end. The human homolog is

the (+) strand of GenBank Accession No. AP000505.1, between allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2).

SEQ ID NO: 207 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E1, distal end. The human homolog is the
5 (-) strand of GenBank Accession No. AC008755.8, C19orf7.

SEQ ID NO: 208 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E2, distal end. The human homolog is the (+) strand of GenBank Accession No. AC058791.4, between LOC346658 and LOC340349.

SEQ ID NO: 209 is a nucleic acid sequence associated with viral, such as Ebola, infection,
10 and is the clone identified as Nucleotide Sequence MV27-E2, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC058791.4, between LOC346658 and LOC340349.

SEQ ID NO: 210 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E3, distal end. The human homolog is the (+) strand of GenBank Accession No. AC079030.13, a region of chromosome 12q21.

15 SEQ ID NO: 211 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV27-E3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC139138.2, between LOC339248 and hypothetical protein FLJ22659.

SEQ ID NO: 212 is a nucleic acid sequence associated with viral, such as Ebola, infection,
20 and is the clone identified as Nucleotide Sequence MV27-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AL513550.9, between SR rich protein DKFZp564B0769 and hypothetical protein MGC14793.

SEQ ID NO: 213 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B1, distal end. The human homolog is the
25 (-) strand of GenBank Accession No. AP001160.4, hypothetical protein FLJ10439.

SEQ ID NO: 214 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-B1, proximal end. The human homolog is the (+) strand of GenBank Accession No. AP001160.4, hypothetical protein FLJ10439.

SEQ ID NO: 215 is a nucleic acid sequence associated with viral, such as Ebola, infection,
30 and is the clone identified as Nucleotide Sequence MV28-B3, distal end. The human homolog is the (+) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 216 is a nucleic acid sequence associated with viral, such as Ebola, infection,
35 and is the clone identified as Nucleotide Sequence MV28-B3, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

SEQ ID NO: 217 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E11, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A.

5   SEQ ID NO: 218 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E11, distal end. The human homolog is the (-) strand of GenBank Accession No. AC090826.15, between cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane

10   anchor, (semaphoring) 7A.

SEQ ID NO: 219 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E1, proximal end. The human homolog is the (-) strand of GenBank Accession No. AC011500.7, ribosomal protein S16 (RPS16).

SEQ ID NO: 220 is a nucleic acid sequence associated with viral, such as Ebola, infection,

15   and is the clone identified as Nucleotide Sequence MV28-E1, distal end. The human homolog is the (+) strand of GenBank Accession No. AC011500.7, ribosomal protein S16 (RPS16).

SEQ ID NO: 221 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E4, distal end. The human homolog is the (-) strand of GenBank Accession No. AC091172.11, between hypothetical protein DKFZp434H0115

20   and ATP citrate lyase (ACLY).

SEQ ID NO: 222 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E4, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC091172.11, between hypothetical protein DKFZp434H0115 and ACLY.

25   SEQ ID NO: 223 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E7, distal end. The human homolog is the (+) strand of GenBank Accession No. AL035594.7, protein tyrosine phosphatase, receptor type, K (PTPRK).

SEQ ID NO: 224 is a nucleic acid sequence associated with viral, such as Ebola, infection,

30   and is the clone identified as Nucleotide Sequence MV28-E7, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC124857.2, calnexin (CANX) and (-) strand of GenBank Accession No. AL035594.7, protein tyrosine phosphatase, receptor type, K (PTPRK).

SEQ ID NO: 225 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E8, distal end. The human homolog is the

35   (+) strand of GenBank Accession No. AC009144.5, cyclin M2 (CNNM2).

SEQ ID NO: 226 is a nucleic acid sequence associated with viral, such as Ebola, infection, and is the clone identified as Nucleotide Sequence MV28-E8, proximal end. The human homolog is the (+) strand of GenBank Accession No. AC011510.7, AXL receptor tyrosine kinase (AXL).

SEQ ID NO: 227 is a nucleic acid sequence showing GenBank Accession No. BC008947, *Homo sapiens* chromosome 10 open reading frame 3, mRNA (cDNA clone MGC:3422 IMAGE:3028566). This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 228 is an amino acid sequence encoded by SEQ ID NO: 227.

SEQ ID NO: 229 is a nucleic acid sequence showing GenBank Accession No. NM_018131, *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3). This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 230 is an amino acid sequence encoded by SEQ ID NO: 229.

SEQ ID NO: 231 is a nucleic acid sequence showing GenBank Accession No. NM_013451, *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*) (FER1L3), transcript variant 1, mRNA. This sequence is associated with viral infection, such as Ebola infection.

SEQ ID NO: 232 is an amino acid sequence encoded by SEQ ID NO: 231.

SEQ ID NOS: 233 and 234 are exemplary complementary primers.

SEQ ID NOS: 235-237 are primer sequences used to sequence the shuttle clones as described in Example 2.

SEQ ID NOS: 238-241 are Rab9 siRNA sequences.

SEQ ID NOS: 242-245 are AXL receptor tyrosine kinase siRNA sequences.

SEQ ID NOS: 246-295 are beta-chimerin receptor tyrosine kinase RNAi sequences.

SEQ ID NOS: 296-345 are retinoblastoma binding protein 1 RNAi sequences.

SEQ ID NOS: 346-395 are *Homo sapiens* chromosome 10 open reading frame 3 RNAi sequences.

SEQ ID NOS: 396-445 are *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*), transcript variant 1 RNAi sequences.

SEQ ID NOS: 446-495 are *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3) RNAi sequences.

SEQ ID NOS: 496-545 are malic enzyme RNAi sequences.

SEQ ID NOS: 546-595 are cadherin related 23 RNAi sequences.

SEQ ID NOS: 596-645 are sideroflexin 5 RNAi sequences.

SEQ ID NOS: 646-695 are polybromo 1 (PB1) RNAi sequences.

SEQ ID NOS: 696-720 are elongation factor for selenoprotein translation RNAi sequences.

SEQ ID NOS: 721-745 are integrin, beta 1 RNAi sequences.

SEQ ID NOS: 746-795 are huntingtin interacting protein 1 RNAi sequences.

SEQ ID NOS: 796-845 are cyclin M2 RNAi sequences.

DETAILED DESCRIPTION OF SEVERAL EMBODIMENTS

Abbreviations and Terms

The following explanations of terms and methods are provided to better describe the present disclosure and to guide those of ordinary skill in the art in the practice of the present disclosure. The singular forms "a," "an," and "the" refer to one or more than one, unless the context clearly dictates

otherwise. For example, the term "comprising a nucleic acid" includes single or plural nucleic acids and is considered equivalent to the phrase "comprising at least one nucleic acid." The term "or" refers to a single element of stated alternative elements or a combination of two or more elements, unless the context clearly indicates otherwise. For example, the phrase "a first nucleic acid or a

5   second nucleic acid" refers to the first nucleic acid, the second nucleic acid, or a combination of both the first and second nucleic acids. As used herein, "comprises" means "includes." Thus, "comprising a promoter and an open reading frame," means "including a promoter and an open reading frame," without excluding additional elements.

Unless explained otherwise, all technical and scientific terms used herein have the same

10   meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present disclosure, suitable methods and materials are described below. The materials, methods, and examples are illustrative only and not intended to be limiting.

15   A = adenine

C = cytosine

DNA = deoxyribonucleic acid

ds = double-stranded (for example, dsDNA)

G = guanine

20   mg = milligram

ng = nanogram

PCR = polymerase chain reaction

Pu = purine

Py = pyrimidine

25   RNA = ribonucleic acid

mRNA = messenger RNA

MOI = multiplicity of infection

siRNA = short interfering or interrupting RNA

ss = single-stranded (for example, ssDNA)

30   T = thymine

T_m = melting temperature

U = uracil

µg = microgram

µl = microliter

35

Amplification of a nucleic acid. To increase the number of copies of a nucleic acid. Several methods can be used to amplify a nucleic acid, such as polymerase chain reaction (PCR). Other examples of amplification include, but are not limited to, strand displacement amplification (U.S. Patent No: 5,744,311); transcription-free isothermal amplification (U.S. Patent No: 6,033,881);

repair chain reaction amplification (WO 90/01069); ligase chain reaction amplification (European Patent Appl. 320 308); gap filling ligase chain reaction amplification (U.S. Patent No: 5,427,930); and NASBA™ RNA transcription-free amplification (U.S. Patent No: 6,025,134).

The amplification products ("amplicons") can be further processed, manipulated, or

5   characterized by electrophoresis, restriction endonuclease digestion, hybridization, nucleic acid sequencing, ligation, or other molecular biology techniques. Standard protocols can be modified. For example, PCR can be modified by using reverse transcriptase PCR (RT-PCR) to amplify RNA molecules.

Antisense, Sense, and Antigene. Antisense molecules are molecules that are specifically

10 hybridizable or specifically complementary to either RNA or the plus strand of DNA. Sense molecules are molecules that are specifically hybridizable or specifically complementary to the minus strand of DNA. Antigene molecules are either antisense or sense molecules directed to a particular dsDNA target. These molecules can be used to interfere with gene expression.

Double-stranded DNA (dsDNA) has two strands, a 5' to 3' strand, referred to as the plus (+)

15 strand, and a 3' to 5' strand (the reverse complement), referred to as the minus (-) strand. Because RNA polymerase adds nucleic acids in a 5' to 3' direction, the minus strand of the DNA serves as the template for the RNA during transcription. Thus, the RNA formed will have a sequence complementary to the minus strand and virtually identical to the plus strand, except that U is substituted for T in RNA molecules.

20 Array. An arrangement of biological samples or molecules, such as an arrangement of tissues, cells, or biological macromolecules (including, but not limited to, peptides or nucleic acids) in addressable locations on or in a substrate. The arrangement of molecules within the array can be regular, such as being arranged in uniform rows and columns, or irregular. The number of addressable locations within the array can vary, for example from a few (such as two or three) to

25 more than 50, 100, 200, 500, 1000, 10,000, or more. In certain examples, the array includes one or more molecules or samples occurring on the array a plurality of times (twice or more) to provide an added feature to the array, such as redundant activity or to provide internal controls. A "microarray" is an array that is miniaturized and evaluated or analyzed using microscopy.

Within an array, each arrayed sample or molecule is addressable, such that its location can

30 be reliably and consistently determined within the at least two dimensions of the array. The location or address of each sample or molecule can be assigned when it is applied to the array, and a key or guide can be provided in order to correlate each location with the appropriate target sample or molecule position. Ordered arrays can be arranged in a symmetrical grid pattern or other patterns, for example, in radially distributed lines, spiral lines, or ordered clusters. Addressable arrays can be

35 computer readable; a computer can be programmed to correlate a particular address on the array with information about the sample at that position, such as hybridization or binding data, including signal intensity. In some exemplary computer readable formats, the individual samples or molecules in the array are arranged regularly (for example, in a Cartesian grid pattern), which can be correlated to address information by a computer.

The sample or molecule addresses on an array can assume many different shapes. For example, substantially square regions can be used as addresses within arrays, but addresses can be differently shaped, for example, substantially rectangular, triangular, oval, irregular, or another shape. The term "spot" refers generally to a localized placement of molecules, tissue or cells, and is not

5   limited to a round or substantially round region or address.

Examples of macroarrays include the Histo™-array and INSTA-blot™ lines of products available from Imgenix, Inc. (San Diego, CA) and the Max Array™ line of products available from Zymed Laboratories, Inc. (South San Francisco, CA), while exemplary microarrays include the various GeneChip® technologies and products available from Affymetrix, Inc. (Santa Clara, CA) and

10 the Hilight™, Label Star™, and Array-Ready Oligo Set lines of products available from Qiagen, Inc. (Valencia, CA).

β-chimerin. The term β-chimerin includes any β-chimerin gene, cDNA, RNA, or protein from any organism and is a β-chimerin that can function as a type of rho-GTPase. In some examples, β-chimerin is involved in viral infection.

15 Rho-GTPases are a family of small GTPases implicated as components of cellular signal transduction cascades. Signals that pass through rho-GTPase cascades can be initiated by the activation of cell surface proteins, such as growth factors. Functions of signaling cascades mediated by rho-GTPases, include, but are not limited to, alterations in cellular morphology which are linked to processes such as immune cell function, oncogenesis, metastasis and certain diseases (Peck, *FEBS*

20 *Lett.* 528:27, 2002).

Examples of native β-chimerin nucleic acid sequences include, but are not limited to those shown in SEQ ID NOS: 21-22 (such as a target sequence associated with SEQ ID NOS: 21-22), as well as the protein sequence encoded thereby. This cell line remains CD4$^+$ after exposure to HIV 1 and HIV 2 and is resistant to HIV infection. β-chimerin also includes variants, fusions, and

25 fragments of the disclosed nucleic acid and amino acid sequences that retain β-chimerin biological activity.

Examples of β-chimerin amino acid sequences include, but are not limited to: Genbank Accession Nos: NM_004067 (mRNA) and NP_004058.1 (protein). In one example, a β-chimerin sequence includes a full-length wild-type (or native) sequence, as well as β-chimerin allelic variants,

30 variants, fragments, homologs or fusion sequences that retain the ability to function as a type of rho-GTPase. In certain examples, β-chimerin has at least 80% sequence identity, for example at least 85%, 90%, 95%, or 98% sequence identity to a native β-chimerin.

cDNA (complementary DNA). A piece of DNA lacking internal, non-coding segments (introns) and transcriptional regulatory sequences. A cDNA also can contain untranslated regions

35 (UTRs) that are responsible for translational control in the corresponding RNA molecule. cDNA can be produced using various methods, such as synthesis in the laboratory by reverse transcription from messenger RNA extracted from cells.

Complementary. Complementary binding occurs when the base of one nucleic acid molecule forms a hydrogen bond the base of another nucleic acid molecule. Normally, the base

28

adenine (A) is complementary to thymidine (T) and uracil (U), while cytosine (C) is complementary to guanine (G). For example, the sequence 5'-ATCG-3' of one ssDNA molecule can bond to 3'-TAGC-5' of another ssDNA to form a dsDNA.

Nucleic acid molecules can be complementary to each other even without complete hydrogen-bonding of all bases of each molecule. By way of example only (and without limitation), the ssDNA: 5'-GCTTGCCAAACCTACA-3' (SEQ ID NO: 233) is considered complementary to the ssDNA 3'-CGAACGGTCTGGATGT-5' (SEQ ID NO: 234) even though there is a mismatched base pair (A-C rather than A-T or G-C) at the ninth position.

Conservative substitution: A substitution of an amino acid residue for another amino acid residue having similar biochemical properties. Typically, conservative substitutions have little to no impact on the biological activity of a resulting polypeptide. In a particular example, a conservative substitution is an amino acid substitution in a peptide that does not substantially affect the biological function of the peptide. A peptide can include one or more amino acid substitutions, for example 2-10 conservative substitutions, 2-5 conservative substitutions, 4-9 conservative substitutions, such as 2, 5 or 10 conservative substitutions.

For example, a conservative substitution in a β-chimerin peptide (such as a peptide encoded by a target sequence associated with SEQ ID NO: 21 or 22) does not substantially affect the ability of β-chimerin to confer resistance to HIV infection. In another example, a conservative substitution in a Rab9 peptide (such as a peptide encoded by a target sequence associated with SEQ ID NOS: 118 or 119) is one that does not substantially affect the ability of Rab9 to confer resistance to infection by a pathogen that can hijack a lipid raft, such as HIV or Ebola.

A polypeptide can be produced to contain one or more conservative substitutions by manipulating the nucleotide sequence that encodes that polypeptide using, for example, standard procedures such as site-directed mutagenesis or PCR. Alternatively, a polypeptide can be produced to contain one or more conservative substitutions by using standard peptide synthesis methods. An alanine scan can be used to identify which amino acid residues in a protein can tolerate an amino acid substitution. In one example, the biological activity of the protein is not decreased by more than 25%, for example not more than 20%, for example not more than 10%, when an alanine, or other conservative amino acid (such as those listed below), is substituted for one or more native amino acids.

Examples of amino acids which can be substituted for an original amino acid in a protein and which are regarded as conservative substitutions include, but are not limited to: Ser for Ala; Lys for Arg; Gln or His for Asn; Glu for Asp; Ser for Cys; Asn for Gln; Asp for Glu; Pro for Gly; Asn or Gln for His; Leu or Val for Ile; Ile or Val for Leu; Arg or Gln for Lys; Leu or Ile for Met; Met, Leu or Tyr for Phe; Thr for Ser; Ser for Thr; Tyr for Trp; Trp or Phe for Tyr; and Ile or Leu for Val.

Further information about conservative substitutions can be found in, among other locations in, Ben-Bassat et al., (J. Bacteriol. 169:751-7, 1987), O'Regan et al., (Gene 77:237-51, 1989), Sahin-

Toth et al., (Protein Sci. 3:240-7, 1994), Hochuli et al., (Bio/Technology 6:1321-5, 1988) and in standard textbooks of genetics and molecular biology.

Ebola virus. A highly contagious hemorrhagic virus named after a river in the Democratic Republic of the Congo (formerly Zaire) in Africa, where it was first recognized. Ebola is one of two

5 members of a family of RNA viruses called the Filoviridae. There are four identified subtypes of Ebola virus. Three of the four have caused disease in humans: Ebola-Zaire, Ebola-Sudan, and Ebola-Ivory Coast. The fourth, Ebola-Reston, has caused disease in nonhuman primates, but not in humans.

Ebola hemorrhagic fever (Ebola HF) is a severe, often fatal disease in humans and nonhuman primates (for example, monkeys, gorillas, and chimpanzees) that is caused by Ebola virus

10 infection. Diagnosing Ebola HF in a recently infected individual can be difficult because early symptoms, such as red eyes and a skin rash, are nonspecific to the virus and are seen in other subjects with diseases that occur much more frequently. Antigen-capture enzyme-linked immunosorbent assay (ELISA) testing, IgM ELISA, PCR, and virus isolation can be used to diagnose a case of Ebola HF within a few days after the onset of symptoms. Subjects tested later in the course of the disease,

15 or after recovery, can be tested for IgM and IgG antibodies. The disease also can be diagnosed retrospectively in deceased patients by using immunohistochemistry testing, virus isolation, or PCR.

Encodes: Unless evident from its context, includes DNA sequences that encode a polypeptide, as the term is typically used, as well as DNA sequences that are transcribed into inhibitory antisense molecules.

20 Expression: With respect to a gene sequence, refers to transcription of the gene and, as appropriate, translation of the resulting mRNA transcript to a protein. Thus, expression of a protein coding sequence results from transcription and translation of the coding sequence.

Functional deletion: A mutation, partial or complete deletion, insertion, or other variation made to a gene sequence that inhibits production of the gene product or renders the gene product non-

25 functional. For example, a functional deletion of a Rab9 gene in a cell results in a cells having non-functional Rab9 protein, which results in the cell having an increase resistance to infection by a pathogen that uses a lipid raft.

Gene. A nucleic acid sequence that encodes a polypeptide under the control of a regulatory sequence, such as a promoter or operator. A gene includes an open reading frame encoding a

30 polypeptide of the present disclosure, as well as exon and (optionally) intron sequences. An intron is a DNA sequence present in a given gene that is not translated into protein and is generally found between exons. The coding sequence of the gene is the portion transcribed and translated into a polypeptide (in vivo, in vitro or in situ) when placed under the control of an appropriate regulatory sequence. The boundaries of the coding sequence can be determined by a start codon at the 5'

35 (amino) terminus and a stop codon at the 3' (carboxyl) terminus. If the coding sequence is intended to be expressed in a eukaryotic cell, a polyadenylation signal and transcription termination sequence can be included 3' to the coding sequence.

Transcriptional and translational control sequences include, but are not limited to, DNA regulatory sequences such as promoters, enhancers, and terminators that provide for the expression of

the coding sequence, such as expression in a host cell. A polyadenylation signal is an exemplary eukaryotic control sequence. A promoter is a regulatory region capable of binding RNA polymerase and initiating transcription of a downstream (3' direction) coding sequence. Additionally, a gene can include a signal sequence at the beginning of the coding sequence of a protein to be secreted or

5 expressed on the surface of a cell. This sequence can encode a signal peptide, N-terminal to the mature polypeptide, which directs the host cell to translocate the polypeptide.

Host Cell. Any cell that can be infected with a virus or other pathogen, such as a bacterium. A host cell can be prokaryotic or eukaryotic, such as a cell from an insect, crustacean, mammal, bird, reptile, yeast, or a bacteria such as *E. coli*. Exemplary host cells include, but are not limited to,

10 mammalian B-lymphocyte cells. Examples of viruses include, but are not limited to HIV, influenza A, and Ebola.

The host cell can be part of an organism, or part of a cell culture, such as a culture of mammalian cells or a bacterial culture. A host nucleic acid is a nucleic acid present in a host cell that expresses a host protein. Decreasing or inhibiting the interaction between a host polypeptide or host

15 nucleic acid and a virus or viral protein can occur *in vitro*, *in vivo*, and *in situ* environments.

Human Immunodeficiency Virus (HIV). A retrovirus that causes immunosuppression in humans and leads to a disease complex known as acquired immunodeficiency syndrome (AIDS). This immunosuppression results from a progressive depletion and functional impairment of T lymphocytes expressing the CD4 cell surface glycoprotein. The loss of CD4 helper/inducer T cell

20 function may underlie the loss of cellular and humoral immunity leading to the opportunistic infections and malignancies seen in AIDS.

Depletion of CD4 T cells results from the ability of HIV to selectively infect, replicate in, and ultimately destroy these T cells (for example see Klatzmann *et al.*, *Science* 225:59, 1984). CD4 itself is an important component, and in some examples an essential component, of the cellular

25 receptor for HIV.

HIV subtypes can be identified by particular number, such as HIV-1 and HIV-2. In the HIV life cycle, the virus enters a host cell in at least three stages: receptor docking, viral-cell membrane fusion, and particle uptake (D'Souza *et al.*, *JAMA* 284:215, 2000). Receptor docking begins with a gp120 component of a virion spike binding to the CD4 receptor on the host cell. Conformational

30 changes in gp120 induced by gp120-CD4 interaction promote an interaction between gp120 and either CCR5 or CXCR4 cellular co-receptors. The gp41 protein then mediates fusion of the viral and target-cell membranes. More detailed information about HIV can be found in Coffin *et al.*, *Retroviruses* (Cold Spring Harbor Laboratory Press, 1997).

Hybridization. Hybridization of a nucleic acid occurs when two complementary nucleic

35 acid molecules undergo an amount of hydrogen bonding to each other. The stringency of hybridization can vary according to the environmental conditions surrounding the nucleic acids, the nature of the hybridization method, and the composition and length of the nucleic acids used. For example, temperature and ionic strength (such as Na^+ concentration) can affect the stringency of hybridization. Calculations regarding hybridization conditions required for attaining particular

degrees of stringency are discussed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 2001); and Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes* Part I, Chapter 2 (Elsevier, New York, 1993).

5   The T_m is the temperature at which 50% of a given strand of nucleic acid is hybridized to its complementary strand. The T_m of a particular nucleic acid can be determined by various methods, such as observing the transition state between a single-stranded and double-stranded state during a temperature change, such as heating a dsDNA from about 30°C to about 100°C, and detecting when the dsDNA denatures to ssDNA. This can be accomplished by determining a melting profile for the

10   nucleic acid. For longer nucleic acid fragments, such as PCR products, the nearest-neighbor method can be used to determine T_m (Breslauer *et al.*, *Proc. Natl. Acad. Sci. USA* 83:3746-50, 1986). Additionally, MeltCalc software can be used to determine T_m (Schütz and von Ahsen, *Biotechniques* 30:8018-24, 1999).

       For purposes of this disclosure, "stringent conditions" encompass conditions under which

15   hybridization only will occur if there is less than 25% mismatch between the hybridization molecule and the target sequence. "Moderate stringency" conditions are those under which molecules with more than 25% sequence mismatch will not hybridize; conditions of "medium stringency" are those under which molecules with more than 15% mismatch will not hybridize, and conditions of "high stringency" are those under which sequences with more than 10% mismatch will not hybridize.

20   Conditions of "very high stringency" are those under which sequences with more than 5% mismatch will not hybridize.

       Moderately stringent hybridization conditions are when the hybridization is performed at about 42°C in a hybridization solution containing 25 mM KPO$_4$ (pH 7.4), 5X SSC, 5X Denhart's solution, 50 µg/mL denatured, sonicated salmon sperm DNA, 50% formamide, 10% Dextran sulfate,

25   and 1-15 ng/mL probe (about 5x10^7 cpm/µg), while the washes are performed at about 50°C with a wash solution containing 2X SSC and 0.1% sodium dodecyl sulfate.

       Highly stringent hybridization conditions are when the hybridization is performed at about 42°C in a hybridization solution containing 25 mM KPO$_4$ (pH 7.4), 5X SSC, 5X Denhart's solution, 50 µg/mL denatured, sonicated salmon sperm DNA, 50% formamide, 10% Dextran sulfate, and 1-15

30   ng/mL probe (about 5x10^7 cpm/µg), while the washes are performed at about 65°C with a wash solution containing 0.2X SSC and 0.1% sodium dodecyl sulfate.

       Infection. The entry, replication, insertion, lysis or other event or process involved with the pathogensis of a virus or other infectious agent into a host cell. Thus, decreasing infection includes decreasing entry, replication, insertion, lysis, or other pathogensis of a virus or other pathogen into a

35   cell or subject, or combinations thereof. Infection includes the introduction of an infectious agent, such as a non-recombinant virus, recombinant virus, plasmid, bacteria, prion, eukaryotic microbe, or other agent capable of infecting a host, such as the cell of a subject.

       In another example, infection is the introduction of a recombinant vector into a host cell via transduction, transformation, transfection, or other method. Vectors include, but are not limited to,

viral, plasmid, cosmid, and artificial chromosome vectors. For example, a recombinant vector can include an antisense molecule, RNAi molecule, or siRNA that recognizes any target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or variants, fusions, or fragments thereof, as well as SEQ ID NOS: 1-227, 229, and 231 themselves.

5   Influenza virus. A virus that causes respiratory disease or influenza ("the flu") and can lead to a secondary infection in the host, such as a bacterial infection of the lungs. Three types of influenza are currently known: influenza A, influenza B, and influenza C. Influenza A is the most common form of the virus and is capable of infection humans and non-human animals, such as pigs, horses, chickens, ducks and other birds.

10   The viral genome includes eight RNA molecules. HA, which encodes hemagglutinin (three hemagglutinin subtypes: H1, H2, and H3); M, which encodes two matrix proteins based on two different open reading frames within the nucleic acid sequence; NA encodes for neuraminidase; NP encodes the nucleoprotein; NS encodes two non-structural proteins based on different open reading frames within the nucleic acid sequence; and three genes that encode RNA polymerases (PA, PB1, 15   PB2). The influenza virus can be categorized into subtypes on the bases of the surface glycoproteins.

The replication cycle of the influenza virus begins with binding of the viral hemagglutinin molecules to the surface carbohydrate of epithelial cell of a host cell, which draws the virus into the cell by receptor-mediated endocytosis. The viral membrane fuses with the endocytotic vesicle membrane, allowing the RNA molecules of the viral genome to enter the interior of the cell where 20   these molecules later enter the cell nucleus and are replicated into viral-complementary RNA and new viral RNA and transcribed into viral mRNA, which are transported into the cytosol where they are translated into the proteins of new viral particles. After viral particles are assembled into new viruses, the neuraminidase glycoproteins proteins aid in the budding of the viruses from the cellular membrane of the host cell, thus releasing new viruses capable of infecting other host cells.

25   Isolated: An "isolated" biological component (such as a nucleic acid or protein) has been substantially separated, produced apart from, or purified away from other biological components in the cell of the organism in which the component naturally occurs, such as other chromosomal and extrachromosomal DNA and RNA, and proteins. Nucleic acids and proteins which have been "isolated" include nucleic acids and proteins purified by standard purification methods. The term 30   also embraces nucleic acids and proteins prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids, proteins and peptides.

Nucleic acid. A deoxyribonucleotide or ribonucleotide polymer in either single (ss) or double stranded (ds) form, and can include analogues of natural nucleotides that hybridize to nucleic acids in a manner similar to naturally occurring nucleotides. In some examples, a nucleic acid is a 35   nucleotide analog.

Unless otherwise specified, any reference to a nucleic acid molecule includes the reverse complement of nucleic acid. Except where single-strandedness is required by the text herein (for example, a ssRNA molecule), any nucleic acid written to depict only a single strand encompasses both strands of a corresponding double-stranded nucleic acid. For example, depiction of a plus-strand

of a dsDNA also encompasses the complementary minus-strand of that dsDNA. Additionally, reference to the nucleic acid molecule that encodes a specific protein, or a fragment thereof, encompasses both the sense strand and its reverse complement.

In particular examples, a nucleic acid includes a nucleotide sequence shown in any of SEQ ID NOS: 1-227, 229, and 231, or a variant, fragment, or fusion thereof. In other examples, a nucleic acid has a nucleotide sequence including a target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a variant, fragment, or fusion thereof, such as the corresponding cDNA or mRNA of SEQ ID NOS: 1-227, 229, and 231.

The fragment can be any portion of the nucleic acid corresponding to at least 5 contiguous bases from any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229, and 231, for example at least 20 contiguous bases, at least 50 contiguous bases, at least 100 contiguous bases, at least 250 contiguous bases, or even at least 500 or more contiguous bases. A fragment can be chosen from a particular portion of any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, such as a particular half, third, fourth, fifth, sixth, seventh, eighth, ninth, tenth, or smaller portion of any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231. Fragments of the nucleic acids described herein can be used as probes and primers.

Oligonucleotide. A linear polynucleotide (such as DNA or RNA) sequence of at least 9 nucleotides, for example at least 15, 18, 24, 25, 30, 50, 100, 200 or even 500 nucleotides long. In particular examples, an oligonucleotide is about 6-50 bases, for example about 10-25 bases, such as 12-20 bases.

An oligonucleotide analog refers to moieties that function similarly to oligonucleotides, but have non-naturally occurring portions. For example, oligonucleotide analogs can contain non-naturally occurring portions, such as altered sugar moieties or inter-sugar linkages, such as a phosphorothioate oligodeoxynucleotide. Functional analogs of naturally occurring polynucleotides can bind to RNA or DNA, and include peptide nucleic acid (PNA) molecules.

Open reading frame (ORF). A series of nucleotide triplets (codons) coding for amino acids without any internal termination codons. These sequences are usually translatable into a peptide.

Operably linked. A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame.

Pathogen: A disease-producing agent. Examples include, but are not limited to viruses, bacteria, and fungi.

Pharmaceutical agent or drug: A chemical compound or composition capable of inducing a desired therapeutic or prophylactic effect when administered to a subject, alone or in combination with another therapeutic agent(s) or pharmaceutically acceptable carriers. In a particular example, a

34

pharmaceutical agent decreases or even inhibits infection of a cell, such as the cell of a subject, by a pathogen, such as a virus.

Polymorphism. A polymorphism exists when two or more versions of a nucleic acid sequence exist within a population of subjects. For example, a polymorphic nucleic acid can be one where the most common allele has a frequency of 99% or less. Different alleles can be identified according to differences in nucleic acid sequences, and genetic variations occurring in more than 1% of a population (which is the commonly accepted frequency for defining polymorphism) are useful polymorphisms for certain applications.

The allelic frequency (the proportion of all allele nucleic acids within a population that are of a specified type) can be determined by directly counting or estimating the number and type of alleles within a population. Polymorphisms and methods of determining allelic frequencies are discussed in Hartl, D.L. and Clark, A.G., Principles of Population Genetics, Third Edition (Sinauer Associates, Inc., Sunderland Massachusetts, 1997), particularly in chapters 1 and 2.

Preventing or treating a disease: "Preventing" a disease refers to inhibiting the full development of a disease, for example preventing development of a viral infection. "Treatment" refers to a therapeutic intervention that ameliorates a sign or symptom of a disease or pathological condition related to a viral infection, such as inhibiting or decreasing viral infection.

Probes and primers. A probe includes an isolated nucleic acid attached to a detectable label or other reporter molecule. Typical labels include, but are not limited to radioactive isotopes, enzyme substrates, co-factors, ligands, chemiluminescent or fluorescent agents, haptens, and enzymes. Methods for labeling and guidance in the choice of labels appropriate for various purposes are discussed for example in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989) and Ausubel et al. (In Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1998).

Primers are short nucleic acid molecules, such as DNA oligonucleotides ten nucleotides or more in length. Longer DNA oligonucleotides can be about 15, 20, 25, 30 or 50 nucleotides or more in length. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then the primer extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, for example by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods.

Nucleic acid probes and primers can be prepared based on the nucleic acid molecules of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, as indicators of resistance to infection. Probes and primers can be based on fragments or portions of these nucleic acid molecules, or on the reverse complement of these sequences, as well as probes and primers to 5' or 3' regions of the nucleic acids.

The specificity of a probe or primer increases with its length. Thus, for example, a primer that includes 30 consecutive nucleotides of a β-chimerin or Rab9 gene will anneal to a target sequence, such as another homolog of a β-chimerin or Rab9 gene, respectively, with a higher specificity than a

corresponding primer of only 15 nucleotides. Thus, to obtain greater specificity, probes and primers can be selected that include at least 20, 25, 30, 35, 40, 45, 50 or more consecutive nucleotides of a nucleic acid disclosed herein.

Protein coding sequence or a sequence that encodes a peptide: A nucleic acid sequence

5   that is transcribed (in the case of DNA) and is translated (in the case of mRNA) into a peptide *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxy) terminus. A coding sequence can include, but is not limited to, cDNA from procaryotic or eukaryotic mRNA, genomic DNA sequences from procaryotic or eukaryotic DNA, and

10   even synthetic DNA sequences. A transcription termination sequence is usually be located 3' to the coding sequence.

Purified. The term purified does not require absolute purity; rather, it is a relative term. Thus, for example, a purified peptide preparation is one in which the peptide or protein is more enriched than the peptide or protein is in its environment within a cell, such that the peptide is

15   substantially separated from cellular components (nucleic acids, lipids, carbohydrates, and other polypeptides) that may accompany it. In another example, a purified peptide preparation is one in which the peptide is substantially-free from contaminants, such as those that might be present following chemical synthesis of the peptide.

In one example, an peptide is purified when at least 60% by weight of a sample is composed

20   of the peptide, for example when 75%, 95%, or 99% or more of a sample is composed of the peptide, such as a β-chimerin or Rab9 peptide. Examples of methods that can be used to purify proteins, include, but are not limited to the methods disclosed in Sambrook et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, New York, 1989, Ch. 17). Protein purity can be determined by, for example, polyacrylamide gel electrophoresis of a protein sample, followed by visualization of

25   a single polypeptide band upon staining the polyacrylamide gel; high-pressure liquid chromatography; sequencing; or other conventional methods.

Rab9: The term Rab9 includes any Rab9 gene, cDNA, RNA, or protein from any organism and that is a Rab9 that can transport late endosomes to trans-golgi and function as a ras-like GTPase. In some examples, Rab9 is involved in lipid raft formation.

30   Examples of native Rab9 nucleic acid sequences include, but are not limited to, target sequences associated with SEQ ID NOS: 118 and 119. Examples of Rab9 amino acid sequences include, but are not limited to: Genbank Accession Nos: BC017265.2 and NM_004251.3 (cDNA) as well as P51151 and AAH17265 (proteins). In one example, a Rab9 sequence includes a full-length wild-type (or native) sequence, as well as Rab9 allelic variants, variants, fragments, homologs or

35   fusion sequences that retain the ability to transport late endosomes to trans-golgi. In certain examples, Rab9 has at least 80% sequence identity, for example at least 85%, 90%, 95%, or 98% sequence identity to a native Rab9.

In other examples, Rab9 has a sequence that hybridizes to a sequence set forth in GenBank Accession No. BC017265.2 or NM_004251.3, and retains Rab9 activity.

Recombinant. A recombinant nucleic acid or protein is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated segments of sequence. This artificial combination can be accomplished, for example, by chemical synthesis or by the artificial manipulation of isolated segments of nucleic acids or proteins, for example, by genetic engineering techniques.

RNA interference (RNAi): A post-transcriptional gene silencing mechanism mediated by double-stranded RNA (dsRNA). Introduction of dsRNA into cells, such as RNAi compounds or siRNA compounds, induces targeted degradation of RNA molecules with homologous sequences. RNAi compounds are typically longer than an siRNA molecule. For example, an RNAi molecule can be at least about 25 nucleic acids, at least about 27 nucleic acids, or even at least about 400 nucleotides in length.

RNAi compounds can be used to modulate transcription, for example, by silencing genes, such as Rab9, β-chimerin, or combinations thereof. In certain examples, an RNAi molecule is directed against a certain target gene, such as Rab9, β-chimerin, or combinations thereof, and is used to decrease viral infection.

Sequence identity: The similarity between nucleic acid or amino acid sequences is expressed in terms of the similarity between the sequences. Sequence identity is frequently measured in terms of percentage identity (or similarity or homology); the higher the percentage, the more similar the two sequences are. Homologs or variants of a protein or nucleic acid disclosed herein, such as target sequences associated with SEQ ID NOS: 1-232, and their corresponding cDNA and protein sequences, will possess a relatively high degree of sequence identity when aligned using standard methods.

Methods of alignment of sequences for comparison are well known in the art. Various programs and alignment algorithms are described in: Smith and Waterman, *Adv. Appl. Math.* 2:482, 1981; Needleman and Wunsch, *J. Mol. Biol.* 48:443, 1970; Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85:2444, 1988; Higgins and Sharp, *Gene* 73:237-44, 1988; Higgins and Sharp, *CABIOS* 5:151-3, 1989; Corpet *et al.*, *Nucl. Acids Res.* 16:10881-90, 1988; Pearson and Lipman, *Proc. Natl. Acad. Sci. U.S.A.* 85:2444, 1988; and Altschul *et al.*, *Nature Genet.* 6:119-29, 1994.

The NCBI Basic Local Alignment Search Tool (BLAST™) (Altschul *et al.*, *J. Mol. Biol.* 215:403-10, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx.

Variants of a peptide, such as a peptide encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, as well as any target sequence associated with SEQ ID NOS: 228, 230, and 232, are typically characterized by possession of at least 70% sequence identity counted over the full length alignment with the amino acid sequence encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, or 231, using the NCBI Blast 2.0, gapped blastp set to default parameters. For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence

cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment is performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed

5   by this method, such as at least 80%, at least 90%, at least 95%, at least 98%, or even at least 99% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs and variants will typically possess at least 80% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85%, at least 90%, at least 95%, or at least 98% depending on their similarity to the reference sequence. Methods for determining

10   sequence identity over such short windows are described at the website that is maintained by the National Center for Biotechnology Information in Bethesda, Maryland. One of skill in the art will appreciate that these sequence identity ranges are provided for guidance only; it is entirely possible that strongly significant homologs could be obtained that fall outside of the ranges provided.

Similar methods can be used to determine the sequence identity between two or more

15   nucleic acids. To compare two nucleic acid sequences, the BLASTN options can be set as follows: -i is set to a file containing the first nucleic acid sequence to be compared (such as C:\seq1.txt); -j is set to a file containing the second nucleic acid sequence to be compared (such as C:\seq2.txt); -p is set to blastn; -o is set to any desired file name (such as C:\output.txt); -q is set to –1; -r is set to 2; and all other options are left at their default setting. For example, the following command can be used to

20   generate an output file containing a comparison between two sequences: C:\Bl2seq –i c:\seq1.txt –j c:\seq2.txt –p blastn –o c:\output.txt –q –1 –r 2.

Once aligned, the number of matches is determined by counting the number of positions where an identical nucleotide or amino acid residue is presented in both sequences. The percent sequence identity is determined by dividing the number of matches either by the length of the

25   sequence set forth in the identified sequence, or by an articulated length (for example, 100 consecutive nucleotides or amino acid residues from a sequence set forth in an identified sequence), followed by multiplying the resulting value by 100. For example, a nucleic acid sequence that has 1166 matches when aligned with a test sequence having 1154 nucleotides is 75.0 percent identical to the test sequence (for example, 1166÷1554*100=75.0). The percent sequence identity value is

30   rounded to the nearest tenth. For example, 75.11, 75.12, 75.13, and 75.14 are rounded down to 75.1, while 75.15, 75.16, 75.17, 75.18, and 75.19 are rounded up to 75.2. The length value will always be an integer. In another example, a target sequence containing a 20-nucleotide region that aligns with 20 consecutive nucleotides from an identified sequence as follows contains a region that shares 75 percent sequence identity to that identified sequence (for example, 15÷20*100=75).

35   1   20
        Target Sequence: AGGTCGTGTACTGTCAGTCA

                                   | || ||| |||| |||| |

        Identified Sequence: ACGTGGTGAACTGCCAGTGA

38

The nucleic acids disclosed herein include nucleic acids have nucleotide sequences that are at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99% identical to the nucleotide sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231. In particular examples, a nucleic acid is substantially similar to the nucleotide
5   sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231. A first nucleic acid is "substantially similar" to a second nucleic acid if, when the first nucleic acid is optimally aligned (with appropriate nucleotide deletions or gap insertions) with the second nucleic acid (or its complementary strand) and there is nucleotide sequence identity of at least about 90%, for example at least about 95%, at least 98% or at least 99% identity. An alternative indication that two nucleic acid
10   molecules are closely related is that the two molecules hybridize to each other under stringent conditions.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences, due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid
15   molecules that all encode substantially the same protein.

Short interfering or interrupting RNA (siRNA). Double-stranded RNAs that can induce sequence-specific post-transcriptional gene silencing, thereby decreasing or even inhibiting gene expression. In some examples, siRNA molecules are about 19-23 nucleotides in length, such as at least 21 nucleotides, for example at least 23 nucleotides.
20   In one example, siRNA triggers the specific degradation of homologous RNA molecules, such as mRNAs, within the region of sequence identity between both the siRNA and the target RNA. For example, WO 02/44321 discloses siRNAs capable of sequence-specific degradation of target mRNAs when base-paired with 3' overhanging ends. The direction of dsRNA processing determines whether a sense or an antisense target RNA can be cleaved by the produced siRNA endonuclease
25   complex. Thus, siRNAs can be used to modulate transcription, for example, by silencing genes, such as Rab9, β-chimerin, or combinations thereof. The effects of siRNAs have been demonstrated in cells from a variety of organisms, including *Drosophila, C. elegans*, insects, frogs, plants, fungi, mice and humans (for example, WO 02/44321; Gitlin *et al., Nature* 418:430-4, 2002; Caplen *et al., Proc. Natl. Acad. Sci.* 98:9742-9747, 2001; and Elbashir *et al., Nature* 411:494-8, 2001).
30   In certain examples, siRNAs are directed against certain target genes, such as Rab9, β-chimerin, or combinations thereof, to confirm results of the gene-trap method used against the same nucleic acid sequence.

Specific binding agent. An agent that binds substantially only to a defined target. For example, a protein-specific binding agent binds substantially only the specified protein and a nucleic
35   acid specific binding agent binds substantially only the specified nucleic acid.

As used herein, the term "protein [X] specific binding agent" includes anti-[X] protein antibodies (including polyclonal or monoclonal antibodies and functional fragments thereof) and other agents (such as soluble receptors) that bind substantially only to the [X] protein. In this context, [X] refers to any specific or designated protein, for instance β-chimerin, Rab9, or any protein listed in Table

1 or encoded by a target sequence associated with SEQ ID NOS: 1-227, 229, and 231 (including variants, fragments, and fusions thereof).

Anti-[X] protein antibodies can be produced using standard procedures such as those described in Harlow and Lane (*Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1998). Antibodies can be polyclonal or monoclonal antibodies, humanized antibodies, Fab fragments, F(ab')2 fragments, single chain antibodies, or chimeric antibodies. For example, polyclonal antibodies can be produced by immunizing a host animal by injection with polypeptides described herein, including the target sequences associated with SEQ ID NOS: 1-227, 229, 231 (or variants, fragments, or fusions thereof). The production of monoclonal antibodies can be
10 accomplished by a variety of methods, such as the hybridoma technique (Kohler and Milstein, *Nature* 256:495-7, 1975), the human B-cell technique (Kosbor *et al.*, *Immunology Today* 4:72, 1983), or the EBV-hybridoma technique (Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96, 1983). Additionally, chimeric antibodies can be produced (for example, see Morrison *et al.*, *J. Bacteriol.* 159:870, 1984; Neuberger *et al.*, *Nature* 312:604-8, 1984; and Takeda *et al.*, *Nature*
15 314:452-4, 1985), as well as single-chain antibodies (for example, see U.S. Pat. Nos: 5,476,786; 5,132,405; and 4,946,778).

The determination that a particular agent binds substantially only to the specified protein readily can be made by using or adapting routine procedures. For example, Western blotting can be used to determine that a given protein binding agent, such as an anti-[X] protein monoclonal antibody,
20 binds substantially only to the [X] protein. Other assays include, but are not limited to, competitive and non-competitive homogenous and heterogeneous enzyme-linked immunosorbent assays (ELISA) as symmetrical or asymmetrical direct or indirect detection formats; "sandwich" immunoassays; immunodiffusion assays; in situ immunoassays (for example, using colloidal gold, enzyme or radioisotope labels); agglutination assays; complement fixing assays; immunoelectrophorectic assays;
25 enzyme-linked immunospot assays (ELISPOT); radioallergosorbent tests (RAST); fluorescent tests, such as used in fluorescent microscopy and flow cytometry; Western, grid, dot or tissue blots; dip-stick assays; halogen assays; or antibody arrays (for example, see O'Meara and Tovey, *Clin. Rev. Allergy Immunol.*, 18:341-95, 2000; Sambrook *et al.*, 2001, Appendix 9; Simonnet and Guilloteau, in: *Methods of Immunological Analysis*, Masseyeff *et al.* (Eds.), VCH, New York, 1993, pp. 270-388).
30 A specific binding agent also can be labeled for direct detection (see Chapter 9, Harlow and Lane, *Antibodies: A Laboratory Manual*. 1988). Suitable labels include (but are not limited to) enzymes (such as alkaline phosphatase (AP) or horseradish peroxidase (HRP)), fluorescent labels, colorimetric labels, radioisotopes, chelating agents, dyes, colloidal gold, ligands (such as biotin), and chemiluminescent agents.
35 Shorter fragments of antibodies can also serve as specific binding agents. For instance, Fabs, Fvs, and single-chain Fvs (SCFvs) that bind to a specified protein would be specific binding agents. These antibody fragments include: (1) Fab, the fragment containing a monovalent antigen-binding fragment of an antibody molecule produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain; (2) Fab', the fragment of an

antibody molecule obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule; (3) (Fab')2, the fragment of the antibody obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; (4) F(ab')2, a dimer of two Fab' fragments held

5   together by two disulfide bonds; (5) Fv, a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and (6) single chain antibody ("SCA"), a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule. Methods of making these fragments are routine. For

10   example, construction of Fab expression libraries permits the rapid and easy identification of monoclonal Fab fragments with the desired specificity for a protein described herein.

Subject: Living multi-cellular vertebrate organisms, including human and veterinary subjects, such as cows, pigs, horses, dogs, cats, birds, reptiles, and fish.

Target sequences associated with SEQ ID NO: When used herein, this phrase refers to

15   any nucleic acid sequence, amino acid sequence, or combination of nucleic acid and amino acid sequences, that are involved in viral infection, and therefore serve as targets for inhibiting viral infection, and which are or include a specified SEQ ID NO, are involved in the expression of the SEQ ID NO, or are peptide (including protein) sequences that are expressed by such specified SEQ ID NO. Although a target sequence may refer to a SEQ ID NO of a sequence obtained from a particular

20   species, the target sequences also include homologues of the sequence from other related species, such as other mammals. For example, the phrase "target sequences associated with SEQ ID NO. X" can refer to the entire gene sequence of which the particular SEQ ID NO X is a part, the appropriate coding sequence, a promoter sequence associated with the gene, or the corresponding protein sequence, as well as variants, fragments, homologues, and fusions thereof that retain the activity of

25   the native sequence.

For example, when using the phrase "sequences associated with SEQ ID NOS: 21-22," this term encompases β-chimerin genomic sequences, endogenous promoter sequences that promote the expression of β-chimerin, coding sequences, and β-chimerin proteins, as well as variants, fragments homologues and fusions thereof that retain the activity of the native sequence. A particular cDNA

30   sequence associated with SEQ ID NOS: 21-22 is provided in GenBank Accession No. NM_004067, and a particular protein sequence associated with SEQ ID NOS: 21-22 is provided in NP_004058.1.

The term "a GenBank Accession No. associated with SEQ ID NO. X" refers to a GenBank Accession No. that includes SEQ ID NO. X, or is a homolog of SEQ ID NO: X from another mammal, for example a human homolog. The GenBank Accession No. may, in some examples, also

35   identify a coding sequence of an open reading frame, and the sequence of the protein encoded by SEQ ID NO. X.

Although sequences are provided herein that encode (or are included within sequences that encode) host proteins that are involved in viral infection, it should be understood that the ultimate goal is to interfere with the activity of the protein that has been identified to be involved in viral

pathogenesis. Such interference can be at either the level of the nucleic acid that encodes the protein (for example by reducing or otherwise disrupting expression of the protein), or at the level of the protein itself (for example by interfering with the activity of the protein, or its interaction with the virus). The disclosure of specific techniques for achieving these goals in particular species should not

5   be interpreted to limit the method to these particular techniques, or to particular species in which the viral interaction is first identified. The identification of the viral interaction in one species indicates the importance of the interaction between the virus and the protein in that species, as well as the interaction of the virus with homologues of that protein in other species.

    Target sequence of a nucleic acid: A portion of a nucleic acid that, upon hybridization to a

10   therapeutically effective oligonucleotide or oligonucleotide analog, results in reduction or even inhibition of infection by an infectious agent. An antisense or a sense molecule can be used to target a portion of dsDNA, since either can interfere with the expression of that portion of the dsDNA. The antisense molecule can bind to the plus strand, and the sense molecule can bind to the minus strand. Thus, target sequences can be ssDNA, dsDNA, and RNA.

15   Therapeutically active molecule: An agent, such as a protein, antibody or nucleic acid, that can decrease expression of a host protein involved in viral infection (such as those listed in Table 1 or target sequences associated with any of SEQ ID NOS: 1-232, or can decrese an interaction between a host protein involved in viral infection and a viral protein, such as HIV, Ebola, or influenza A, as measured by clinical response (for example, a decrease in infection by a virus, such as an

20   inhibition of infection). Therapeutically active agents also include organic or other chemical compounds that mimic the effects of the therapeutically effective peptide or nucleic acids.

    Therapeutically Effective Amount: An amount of a pharmaceutical preparation that alone, or together with an additional therapeutic agent(s), induces the desired response. The preparations disclosed herein are administered in therapeutically effective amounts.

25   In one example, a desired response is to decrease or inhibit viral infection of a cell, such as a cell of a subject. Viral infection does not need to be completely inhibited for the pharmaceutical preparation to be effective. For example, a pharmaceutical preparation can decrease viral infection by a desired amount, for example by at least 20%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or even at least 100%, as compared to an amount of

30   viral infection in the absence of the pharmaceutical preparation. This decrease or inhibition can result in halting or slowing the progression of, or inducing a regression of a pathological condition caused by the viral infection, or which is capable of relieving signs or symptoms caused by the condition.

    In another or additional example, it is an amount sufficient to partially or completely alleviate symptoms of viral infection within a host subject. Treatment can involve only slowing the

35   progression of the infection temporarily, but can also include halting or reversing the progression of the infection permanently.

    Effective amounts of the therapeutic agents described herein can be determined in many different ways, such as assaying for a reduction in the rate of infection of cells or subjects, a reduction in the viral load within a host, improvement of physiological condition of an infected subject, or

42

increased resistance to infection following exposure to the virus. Effective amounts also can be determined through various *in vitro*, *in vivo* or *in situ* assays, including the assays described herein.

The disclosed therapeutic agents can be administered in a single dose, or in several doses, for example daily, during a course of treatment. However, the effective amount of can be dependent

5   on the source applied (for example a nucleic acid isolated from a cellular extract versus a chemically synthesized and purified nucleic acid), the subject being treated, the severity and type of the condition being treated, and the manner of administration. In addition, the disclosed therapeutic agents can be administered alone, or in the presence of a pharmaceutically acceptable carrier, or in the presence of other therapeutic agents, for example other anti-viral agents.

10   Transduced and Transformed: A virus or vector "transduces" or "transfects" a cell when it transfers nucleic acid into the cell. A cell is "transformed" by a nucleic acid transduced into the cell when the DNA becomes stably replicated by the cell, either by incorporation of the nucleic acid into the cellular genome, or by episomal replication. As used herein, the term transformation encompasses all techniques by which a nucleic acid molecule might be introduced into such a cell,

15   including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Transfected: A transfected cell is a cell into which has been introduced a nucleic acid molecule by molecular biology techniques. The term transfection encompasses all techniques by which a nucleic acid molecule can be introduced into such a cell, including transfection with viral

20   vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration.

Transgene: An exogenous nucleic acid sequence supplied by a vector. In one example, a transgene includes any target sequence associated with SEQ ID NOS: 1-227, 229, 231 (or variants, fragments, or fusions thereof), for example a nucleic acid that encodes a beta-chimerin or Rab9.

25   Variants, fragments or fusions: The disclosed nucleic acid sequences, such as target sequences associated with SEQ ID NOS: 1-227, 229, and 231, and the proteins encoded thereby, include variants, fragments, and fusions thereof that retain the native biological activity (such as playing a role in viral infection). DNA sequences which encode for a protein or fusion thereof, or a fragment or variant of thereof can be engineered to allow the protein to be expressed in eukaryotic

30   cells or organisms, bacteria, insects, and/or plants. To obtain expression, the DNA sequence can be altered and operably linked to other regulatory sequences. The final product, which contains the regulatory sequences and the therapeutic protein, is referred to as a vector. This vector can be introduced into eukaryotic, bacteria, insect, and/or plant cells. Once inside the cell the vector allows the protein to be produced.

35   One of ordinary skill in the art will appreciate that the DNA can be altered in numerous ways without affecting the biological activity of the encoded protein. For example, PCR can be used to produce variations in the DNA sequence which encodes a protein. Such variants can be variants optimized for codon preference in a host cell used to express the protein, or other sequence changes that facilitate expression.

43

Vector: A nucleic acid molecule as introduced into a host cell, thereby producing a
transformed host cell. A vector can include nucleic acid sequences that permit it to replicate in a host
cell, such as an origin of replication, and can also include one or more selectable marker genes and
other genetic elements. An insertional vector is capable of inserting itself into a host nucleic acid.

5   For example, recombinant lambda-phage vectors of host genomes (Coffin *et al.*, *Retroviruses*,
Chapter 5).

Wild-type. A naturally occurring, non-mutated version of a nucleic acid sequence. Among
multiple alleles, the allele with the greatest frequency within the population is usually (but not
necessarily) the wild-type. The term "native" can be used as a synonym for "wild-type."

10

Nucleic Acids and Proteins Involved in Viral Infection

Examples of host nucleic acids and proteins that play a role in viral infection have been
identified and are summarized in Table 1. These nucleic acids and proteins offer new targets for
therapies that reduce or even inhibit or prevent viral infection, and offer new strategies for assessing

15   the risk of infection among certain populations. While the target genes were identified in an assay
using the recited virus, it is appreciated that infections agents such as viruses will share common
pathways. Thus, the host sequences set forth below can be interfered with to decrease infection in a
host cell.

Examples of viruses that can be inhibited are described in Virology, Volumes 1 and 2 by

20   Bernard Fields, Second Edition, 1990, Raven Press. Exemplary viruses include, but are not limited to
members of the family: Picornaviridae (such as Poliovirus, Coxsackievirus, Echovirus ,Rhinovirus,
and Hepatitis A and E); Calciviridae (such as Norwalk and related viruses); Togaviridae and
Flavivirdae (such as hepatitis C, Alphavirus, and Rubella); Coronaviridae (such as SARS);
Rhabdoviridae (such as Rabies); Filoviridae (such as Marburg and Ebola); Paramyxoviridae (such as

25   Parainfluenza, Mumps, Measles, Hydra and Respiratory Synctial virus); Orthomyxoviridae;
Bunyaviridae (including all subtypes and strains); Arenaviridae (such as lymphocytic
choreomeningitis virus and lassa fever and related viruses); Reoviridae (such as Reovirus and
Rotavirus); Retroviridae (such as HTLV, HIV, and Lentivirus); Papoviridae (such as Polyoma and
Papilloma); Adenoviridae (such as Adenovirus); Parvoviridae (such as Parvovirus); Herpesviridae

30   (such as Herpes 1 and 2, Cytomegalovirus, Varicella-Zoster, Kaposi sarcoma related virus (HHV9),
Epstein Barr Virus, and HHV6-7 (roseolavirus)); Poxviridae (such as Pox); Hepadnaviridae (such as
Hepatitis B); as well as Hepatitis D virus, Hanta virus, and newly identified infectious agents.

Table 1: Examples of Host Genes and Protiens Implicated in Pathogenesis

Nucleic Acid or Protein	Associated Virus	SEQ ID NO:	GenBank Accession Nos for cDNA and Protein
T-cell receptor V beta chain	HIV	1-19	

44

T-cell receptor V-D-J beta 2.1 chain	HIV	20	
β-chimerin (CHN2)	HIV	21-22	NM_004067; NP_004058.1
Malic enzyme 1 (ME1)	HIV and Influenza A	23	BC025246; AAH25246.1
Hypothetical protein XP_174419	HIV and Influenza A	24	
sequence from Chromosome 4q31.3-32	HIV and Influenza A	25-27	
alpha satellite DNA	HIV	28	
LOC253788 and LOC219938; coagulation factor III (F3) and LOC91759	HIV	29	
similar to KOX4 (LOC131880) and LOC166140	HIV	30	
LOC222474 and similar to Rho guanine nucleotide exchange factor 4, isoform a, APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta	HIV	31	
ribosomal protein L7A-like 4 (RPL7AL4) and v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC)	HIV	32	
KIAA0564	HIV	33	
alpha satellite DNA; M96 protein	HIV	34	
hypothetical protein similar to G proteins, especially RAP-2A (LOC57826); LOC161005 and osteoblast specific factor 2 (fasciclin I-like; OSF-2)	HIV	35	
Canis familiaris T-cell leukemia translocation-associated (TCTA) gene, aminomethyltransferase (AMT) gene, dystroglycan (DAG1) gene, and bassoon (BSN) gene	Influenza A	36-37	
LIM domain containing preferred translocation partner in lipoma (LPP)	Influenza A	38-48	
sequence between LOC253121 and hyaluronan synthase 2 (HAS2)	Influenza A	49	
Testin 2 and Testin 3 (TES)	Influenza A	50-57	
PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1	Influenza A	58-59	
sequence between LOC149360 and LOC253961	Influenza A	60	
sequence between KIAA1560 and Tectorin beta (TECTB)	Influenza A	61	
Cadherin related 23 (CDH23)	Influenza A	62	BC032581; AAH32581.1
Myeloid/lymphoma or mixed lineage leukemia, translocated to 10 (MMLT10)	Influenza A	63	

45

exportin 5 (XPO5) and DNA polymerase eta (POLH)	Ebola	64-66	
heterogenous nuclear riboprotein C (C1/C2) (HNRPC)	Ebola	67-75	
alpha-endosulfine pseudogene (ENSAP) and LOC128741	Ebola	76	
LOC222888	Ebola	77	
LOC138421 and zinc finger protein 297B (ZNF297B)	Ebola	78	
sideroflexin 5 (SFXN5)	Ebola	79	AY044437; AAK95826
importin 9 (FLJ10402)	Ebola	80	
T-cell receptor beta	Ebola	81-82	
similar to murine putative transcription factor ZNF131 (LOC135952)	Ebola	83-99	
KIAA1259	Ebola	100-101	AB033085; NP_115572
MURR1 and CCT4	Ebola	102	
FLJ40773 and similar to ribosomal protein L24-like (LOC149360)	Ebola	103	
Testin 2 and 3 (TES)	Ebola	104-107	See above
polybromo 1 (PB1)	Ebola	108	NM_018165.2; NP_060635
DNA damage inducible transcript 3 (DDIT3) and KIAA1887	Ebola	109	
PDZ and LIM domain 1 (elfin) (PDLIM1)	Ebola	110	
LOC284803	Ebola	111-112	
PRO0097 and FLJ31958	Ebola	113	
small inducible cytokine E, member 1 (endothelial monocyte-activating) (SCYE1)	Ebola	114-116	
E3 ubiquitin ligase (SMURF2) and MGC40489	Ebola	117-119	
Ras oncogene family member Rab9	Ebola	118-119	
PRO1617 and retinoblastoma binding protein 1 (RBBP1)	Ebola	120-122	NM_000321; NP_000312.1
region of chromosome 2q12	Ebola	123	
elongation factor for selenoprotein translation	Ebola	124	NM_021937.1 NP_068756.1
Transcription factor SMIF (HSA275986)	Ebola	125-137	
KIAA1026	Ebola	138	
trinucleotide repeat containing 5 (TNRC5)	Ebola	139	
homogentisate 1,2-dioxygenase (HGD)	Ebola	140	
region of chromosome Xq23-24	Ebola	141	
region of chromosome 4p15.3	Ebola	142	
similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883)	Ebola	143	

region of chromosome 2q21	Ebola	144	
region of chromosome Xp11.4, including UPS9X	Ebola	145	
LOC221829	Ebola	146	
U3 small nuclear RNA	Ebola	147-154	
integrin, beta 1 (ITGB1)	Ebola	155-158	BC020057; AAH20057.1
acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1)	Ebola	159	
prospero-related homeobox 1 (PROX1)	Ebola	160	
FLJ20627 and FLJ12910	Ebola	161-173	
PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7)	Ebola	174	
LOC131920	Ebola	175	
region of chromosome 13q14	Ebola	176	
neurotrophic tyrosine kinase, receptor, type 3 (NTRK3)	Ebola	177	
TERA protein and FLJ13224	Ebola	178-179	
LOC284260	Ebola	180	
POM (POM121 homolog) and ZP3 fusion (POMZP3)	Ebola	181-182	
DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064)	Ebola	183	
LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7)	Ebola	184-186	
Mus musculus 5S rRNA pseudogene (Rn5s-ps1)	Ebola	187	
ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2)	Ebola	188-192	
Down's syndrome cell adhesion molecule like 1 (DSCAML1)	Ebola	193	
LOC148529	Ebola	194	
Huntingtin-associated protein interacting protein (HAPIP)	Ebola	195	NM_005338.4; NP_005329.3
LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366)	Ebola	196-200	
hypothetical protein FLJ12910	Ebola	201-204	
LOC350411	Ebola	205	
allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2)	Ebola	206	
C10orf7	Ebola	207	
LOC346658 and LOC340349	Ebola	208-209	
region of chromosome 12q21	Ebola	210	
LOC339248 and FLJ22659	Ebola	211	
SR rich protein DKFZp564B0769 and	Ebola	212	

hypothetical protein MGC14793			
FLJ10439	Ebola	213-214	NM_018093.1; NP_060563.1
cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A	Ebola	215-218	
ribosomal protein S16 (RPS16)	Ebola	219-220	BC004324.2; AAH04324.1
hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY)	Ebola	221-222	
calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK)	Ebola	223-224	
cyclin M2 (CNNM2)	Ebola	225	NM_017649.2; NP_060119.2
AXL receptor tyrosine kinase (AXL)	Ebola	226	BC032229; AAH32229.1
Homo sapiens chromosome 10 open reading frame 3	Ebola	227-228	
Homo sapiens chromosome 10 open reading frame 3 (C10orf3)	Ebola	229-230	
Homo sapiens fer-1-like 3, myoferlin (*C. elegans*)	Ebola	231-232	NM_013451.; NP_038479.1

Some of the host nucleic acids described in Table 1 and target sequences associated with SEQ ID NOS: 1-227, 229, and 231 encode polypeptides that are receptors or ligands recognized by a particular virus, such as HIV, influenza A, or the Ebola virus. For example, the T-cell receptor V

5   beta and V-D-J beta 2.1 chain polypeptides are part of the T-cell receptor complex that are recognized by certain glycoproteins in the HIV envelope. Other host nucleic acids encode polypeptides that provide an enzymatic function related to a viral life cycle, such as the signaling pathways controlling viral packaging or enzymes involved in viral replications. For example, the β-chimerin rho-GTPase may mediate a cellular signal that initiates or triggers a process leading to

10 passage of an HIV viral particle into the host cell. The data presented herein indicate that Rab9 is involved in pathogen infectivity, for example by interfering with trafficking of proteins and lipids within cells. In particular examples, it is demonstrated that Rab9 is involved in lipid raft formation, and that decreasing functional Rab9 and lipid rafts decreases the ability of pathogens, such as viruses and bacteria, that hijack lipid rafts to bud or be infectious.

15 Still other host nucleic acids participate in the life cycle of a virus. For example, a certain nucleotide sequence of a host nucleic acid, such as a gene within the host genome can be recognized during insertion and integration of a viral genome (reverse transcribed into DNA from the viral RNA genomic template) into the host genome. Viral integration is described in, for example, Coffin et al., *Retroviruses*, Chapter 5.

20 The nucleic acids and proteins disclosed herein can be identified, isolated, and characterized using any number of techniques of molecular biology, including the specific methods and protocols described herein, such as in the examples below. In some examples, the nucleic acids were identified

and isolated using the Lexicon Genetics, Inc. (The Woodlands, TX) "gene trap" technology disclosed in U.S. Pat. Nos: 6,080,576; 6,136,566; 6,207,371; 6,139,833; 6,218,123 and 6,448,000.

Gene trap technology is a powerful method for cloning and identifying functional genes, as it marks a gene with a tag and simultaneously generates a corresponding genetic variation for that

5   particular locus. The method involves introducing into a cell a DNA construct that can monitor and potentially disrupt the transcriptional activity of the region of the cell's genome into which it is inserted. The gene-trap method used to identify the host sequences is disclosed in U.S. Patent No. 6,448,000 (herein incorporated by reference).

Briefly, the gene trap protocol involves infecting a host cell (for example, a cell of a Sup T-1

10   cell line (human), MDCK cells (canine), or Vero cells (monkey)) with a recombinant vector (for example, U3neoSV1, FIG. 1). The recombinant vector includes a selectable marker or other sequence capable of being used to select infected host cells. However, the selectable marker or other sequence does not have a promoter at its 5' end. An exemplary selectable marker is a nucleic acid encoding resistance to an antibiotic (such as neomycin). A summary of the gene trap method is

15   provided in FIGS. 2 and 3. Infection of the host cell is performed in culture under conditions that yield about one copy of the vector per cell. The vector incorporates into the host cell genome adjacent to an active promoter and interrupts or disrupts the transcription of a nucleic acid in the host cell (FIG. 2). The host promoter drives expression of the selectable marker or other sequence on the vector, and infected cells can then be selected. For example, if the vector carries a nucleic acid

20   encoding neomycin resistance, cells can be selected on a medium that contains neomycin or G418, the neomycin analog for mammalian cells, depending on the type of host cell used.

The selected host cells are expanded in culture to form a library of cells that contain randomly disrupted host genes (FIG. 3). An aliquot of the library of cells is exposed to the appropriate virus, such as HIV, influenza A, or Ebola, to determine the effect of the disrupted host

25   sequence on viral infection of the host cells. Host cells that survive the viral infection, or are relatively resistant to such infection (such as those cells that survive for a longer period of time than about at least 50% of the infected cells), can include one or more disrupted genes involved in viral infection. Thus, by using the vector one can decrease viral or pathogenic infection of a host cell or in a subject. Therefore, by identifying these disrupted genes that decreased or otherwise interfered with

30   viral infection of the host cell, candidate sequences are identified that can be used as targets to decrease or inhibit viral infection.

Those host cells that survive viral infection, or are relatively resistant to such infection, are cloned, for example, by limit dilution using a chambered plate or by growth on methylcellulose. The interrupted host nucleic acid is identified using standard molecular biology methods. For example,

35   host DNA can be isolated from the cell and digested using an appropriate restriction enzyme to free the 5' and 3' sequences adjacent the incorporated vector. The isolated DNA fragment can then be amplified, for example using PCR or by introducing the DNA fragment into a bacterial host cell then growing the bacteria. Once isolated, the host nucleic acid can be further characterized and analyzed.

For example, the nucleic acid can be sequenced and compared to other similar nucleic acids. Methods of using these nucleic acids, and the proteins encoded thereby, are discussed below.

     Using these gene trap methods, several host molecules were identified that were previously not known to be involved in viral pathogenesis (SEQ ID NOS: 1-232, Table 1, and target sequences associated with SEQ ID NOS: 1-232). For example, the AMT gene (target sequences associated with SEQ ID NOS: 36 and 37) participates in influenza A infection of host cells. Fragments of host sequences involved in viral infection and pathogenesis can now be identified, even including fragments or sequences that were previously known to be important in the pathogenesis of intracellular pathogens. For example, although the T-cell receptor was previously implicated in HIV infection, the results disclosed herein demonstrate that the T-cell receptor V-D-J beta 2.1 chain (target sequences associated with SEQ ID NO: 20) is involved and in some examples required for HIV infection, and host cells lacking the T-cell receptor V-D-J beta 2.1 chain are unexpectedly highly resistant to HIV infection. Hence the V-D-J beta 2.1 chain is a target for anti-viral therapy at the DNA or polypeptide level, and other pathogenically active subcomponents of other known pathogenic sequences can also be identified with this method.

     Examples of these host nucleic acid molecules are target sequences associated with SEQ ID NOS: 1-227, 229, and 231 (including variants, fragments, and fusions thereof) and summarized in Table 1. In addition to these specifically disclosed nucleotide sequences, a host nucleic acid can include nucleotide sequences that are similar to any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, such as having at least 70% identity, at least 80% identity, at least 85% identity, at least 90% identity, at least 95% identity, at least 98% identity, or even at least 99% identity to any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231. The disclosed host nucleic acid sequences, and methods of using them, may comprise, consist, or consist essentially of any of the disclosed nucleic acid sequences shown in SEQ ID NOS: 1-227, 229, and 231, as well as target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or variants or fragments thereof, or sequences that hybridize to the identified sequences under stringent or moderately stringent conditions.

     The host nucleic acid molecules also include a fragment of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, such as a probe or primer as described below.

     Host polypeptides corresponding to these nucleic acids also can be used to practice the disclosed methods. In some examples, the polypeptide includes an amino acid sequence that corresponds to a coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a target protein sequence associated with SEQ ID NOS: 228, 230, and 232. However, host polypeptides can also include those having similar amino acid sequences, such as polypeptides that are at least 70% identical, at least 80% identical, at least 90% identical, at least 95% identical, at least 98% identical, or at least 99% identical to the amino acid sequences corresponding to translations of the coding sequence of any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a target protein sequence associated with SEQ ID NOS: 228, 230, and 232. For example, the disclosed host polypeptides and methods of using them, may comprise, consist, or consist

essentially of an amino acid sequence corresponding to a translation of the nucleotide sequence in any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, a target protein sequence associated with SEQ ID NOS: 228, 230, and 232, or any of the protein sequences listed in Table 1. Alternatively, the polypeptides include homologous polypeptides from other mammals (for example

5   human, monkeys, and dogs).

The host polypeptide can have an amino acid sequence that varies by one or more conservative substitutions from the amino acid sequences of the proteins encoded by target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or from the target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232. In one example, there is no more than 1, 2, 3, 4, 5,

10   or 10 conservative amino acid substitutions. In another example, there are 1, 2, 3, 4, 5 or 10 conservative amino acid substitutions. The effects of these amino acid substitutions, deletions, or additions on host polypeptides can be assayed, for example, by analyzing the ability of cells transformed with the derivative proteins to resist infection by the corresponding virus.

Also included are fragments of any host polypeptide encoded by any of the target sequences

15   associated with SEQ ID NOS: 1-227, 229, and 231, as well as fragments of the target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232. For example, a protein can include at least 5-500 contiguous amino acids of the protein, such as at least 6-200, at least 6-100, at least 10-100, at least 10-50, or at least 20-50 contiguous amino acids of the protein. A host polypeptide fragment can be at least 5, at least 10, at least 15, at least 25, at least 50, at least 100, at least 200, at

20   least 500, or more amino acids of a polypeptide having an amino acid sequence corresponding to a coding region of the nucleotide sequence in any of the target sequences associated with SEQ ID NOS: 1-227, 229, and 231, or a conservative variant thereof, as well as target amino acid sequences associated with SEQ ID NOS: 228, 230, and 232.

Fragments of a nucleic acid target sequences associated with SEQ ID NOS: 1-227, 229, and

25   231 can include 10-5000 contiguous nucleic acids, such as 12-1000, 12-500, 15-100, or 18-50 contiguous nucleic acids. A host nucleic acid fragment can be at least at least 5, at least 10, at least 15, at least 20, at least 25, at least 50, at least 100, at least 200, at least 500, at least 1000, at least 2000, at least 5000 or more contiguous nucleic acids in any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a variant or fusion thereof.

30   Also included are host nucleic acids that encode the same polypeptide encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, or a conservative variant of the polypeptide, or a fragment thereof. For example, a host nucleic acid provided by target sequences associated with SEQ ID NOS: 36-37 encodes AMT. A second host nucleic acid also can encode an AMT having the same amino acid sequence as the AMT encoded by target sequences associated with

35   SEQ ID NOS: 36-37, a conservative variant of this AMT, or a fragment thereof, yet this second host nucleic acid can have a different nucleotide sequence than a target sequence associated with SEQ ID NOS: 36-37 due to the degeneracy of the genetic code.

Methods of Using Host Sequences to Decrease Viral Infection

The interaction between a host nucleic acid or polypeptide (such as target sequences associated with SEQ ID NOS: 1-232 and those shown in Table 1) and a virus or viral protein can be decreased or inhibited using the methods provided. Decreasing or inhibiting this interaction can be

5   used to decrease viral infection of a host cell, and/or to decrease symptoms associated with a viral infection in a subject. For example, decreasing or even inhibiting the interaction of a host nucleic acid or polypeptide and a virus can decrease, inhibit, or even prevent infection of a host cell by that virus, or otherwise inhibit the progression or clinical manifestation of the viral infection. In addition, decreasing the interaction of a host nucleic acid or polypeptide and a virus can reduce or alleviate one

10   or more symptoms associated with viral infection, such as a fever.

Several methods can be used to decrease or inhibit the interaction between a viral protein and a host protein or nucleic acid. The viral and host proteins or nucleic acids can be part of an *in vitro* solution, an *in vivo* expression system, or *in situ* with a host tissue or subject. The viral protein can be part of a larger molecule or complex, such as an envelope protein on the envelope of a mature

15   virus or a fragment of a viral envelope. The host protein also can be part of a larger molecule or complex, such as a host polypeptide expressed as part of a fusion protein or contained as one subunit of a larger protein, such as a transport protein, cell receptor, structural protein, or an enzyme. A host nucleic acid can be part of a larger molecule, complex, organism or microorganism such as a host nucleic acid contained within its host genome, a recombinant vector, or a transgenic organism or

20   microorganism (including both extrachromosomal molecules or genomic insertions).

In accordance with the disclosed methods, interaction is decreased or inhibited between a virus or viral protein and more than one (such as 2 or more, such as 3 or more) host nucleic acids or polypeptides. Decreasing or inhibiting the interactions of one or more host nucleic acids or polypeptides with one or more viral proteins can have additive or exponentially increasing effects.

25   For example, it is believed that decreasing the interaction between a host T-cell receptor V-D-J beta 2.1 chain and HIV, or decreasing the activity of a host β-chimerin, within a host cell can enhance the inhibitory effect on HIV infection of that host cell compared to inhibiting the interaction of only one of the host polypeptides. Hence, the methods include interfering with an interaction between the virus or viral protein and more than one of the proteins associated with infection by the same virus.

30   For example, for infection with HIV, the method could interfere with one, or two or more (such as three or more) of the following: T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β-chimerin (CHN2); malic enzyme 1; Hypothetical protein XP_174419; sequence from Chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine

35   nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (such as RAP-2A; LOC57826); LOC161005 and osteoblast specific factor 2 (fasciclin I-like).

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For Ebola virus, examples of targets include one, or two or more (such as three or more) of the following: exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9; T-cell receptor beta; similar to murine putative transcription factor

5   ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773 and similar to ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3 (DDIT3); KIAA1887; PDZ and LIM domain 1 (elfin) (PDLIM1); LOC284803; PRO0097 and FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2) and MGC40489; Rab9; PRO1617 and retinoblastoma binding protein 1 (RBBP1); region of

10   chromosome 2q12; elongation factor for selenoprotein translation; transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5; homogentisate 1,2-dioxygenase; region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829; U3 small nuclear RNA; integrin, beta 1; acrosomal vesicle

15   protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein; FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29

20   (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); 5S rRNA pseudogene; ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1; LOC148529; Huntingtin-associated protein interacting protein; LOC158525 and similar to RIKEN cDNA 1210001E11

25   (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1); HLA-B associated transcript 2 (BAT2); C10orf7 ;LOC346658; LOC340349; region of chromosome 12q21; LOC339248; FLJ22659; SR rich protein DKFZp564B0769; hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1; sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16; hypothetical

30   protein DKFZp434H0115; ATP citrate lyase; calnexin; protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2; AXL receptor tyrosine kinase; *Homo sapiens* chromosome 10 open reading frame 3, mRNA (cDNA clone MGC:3422 IMAGE:3028566); *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3); and *Homo sapiens* fer-1-like 3, myoferlin (*C. elegans*) (FER1L3), transcript variant 1.

35   For influenza, examples of targets include one, or two or more (such as three or more) of the following: T-cell leukemia translocation-associated (TCTA) gene, aminomethyltransferase; dystroglycan; BSN; LIM domain containing preferred translocation partner in lipoma (LPP); sequence between LOC253121 and hyaluronan synthase 2 (HAS2); testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961;

sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; malic enzyme 1; hypothetical protein XP_174419; and sequence from chromosome 4q31.3-32.

5   In examples where a host polypeptide is a cell receptor or part of a cell receptor, decreasing or preventing expression of the polypeptide, or altering the three-dimensional structure of the polypeptide, can reduce or inhibit the interaction between the host cell receptor and a viral protein. Similarly, decreasing, inhibiting or preventing expression of a host ligand polypeptide (or altering the structure of such a ligand) can decrease or inhibit an interaction between the viral protein and the ligand. For example, decreasing or inhibiting expression of one or more enzymes involved in viral

10   pathogenesis, such as those listed in Table 1 and those target sequences associated with SEQ ID NOS: 1-232, can block a component of the viral life cycle, such as blocking a signal pathway leading to transcription or translation of the viral genome, or assembly of viral sub-parts. Decreasing or inhibiting the enzymatic activity of an enzyme (rather than its expression) can have a similar effect.

       Altering the nucleotide sequence of a host nucleic acid, for example by targeting disruption

15   of the nucleotide sequence using complementary nucleic acid sequences, can decrease, inhibit or prevent integration of a viral nucleic acid into the host nucleic acid. Methods that can be used to interrupt or alter translation of a host nucleic acid include, but are not limited to, using an antisense RNA, RNAi molecule, or an siRNA that binds to a messenger RNA transcribed by the nucleic acid encoding a host polypeptide as described herein. Decreasing or inhibiting the expression of the host

20   nucleic acid can also alter the course of the disease. In one example, altering the nucleotide sequence of a host gene that is targeted by a virus for viral integration can decrease, inhibit, or even prevent, integration of that virus into the host genome.

       A host nucleic acid involved in viral infection, including variants, fusions and fragments thereof, can be used to design agents that bind to a target sequence of that nucleic acid, such as

25   antisense nucleic acids or siRNAs. Such nucleic acid binding agents can be used to decrease or inhibit expression of the nucleic acid, to reduce the incidence of viral infection. For example, an expression vector that transcribes antisense RNA or siRNA that recognizes human β-chimerin mRNA is used to transform cell lines obtained from simians. These transformed cell lines are analyzed for infection by simian immunodeficiency virus (SIV), which is related to HIV. If those cells are

30   resistant to SIV infection, the disrupted gene is identified, sequenced, and compared to the human β-chimerin gene. Sequence similarities between the two genes will offer insight into common molecular mechanisms for infection by HIV and SIV, for example, common structural regions within their respective translated proteins.

       A binding agent that recognizes a host nucleic acid involved in viral infection can be used

35   for prophylactic or therapeutic purposes. For example, expression vectors having antisense RNA, RNAi molecules, or siRNA molecules that target a host nucleic acid involved in viral infection, such as β-chimerin, are introduced into the bone marrow of a subject. Uptake of the vector and expression of the antisense RNA, RNAi, or siRNA within cells infected by HIV offers a prophylactic or therapeutic effect by disrupting the β-chimerin genes within those cells, thus decreasing or inhibiting

54

HIV infection. Similarly, expression vectors including Rab9 antisense RNA, RNAi, or siRNA molecules can be introduced into the bone marrow of a subject. Uptake of the vector and expression of Rab9 antisense RNA, RNAi, or siRNA within cells infected by a pathogen that can hijack a lipid raft, such as HIV or Ebola, offers a prophylactic or therapeutic effect by disrupting the Rab9 genes

5   within those cells, thus decreasing or even inhibiting infection by a pathogen that can hijack a lipid raft. The vector, or other nucleic acid carrying the nucleic acid specific binding agent, is introduced into a subject by any standard molecular biology method and can be included in a composition containing a pharmaceutically acceptable carrier.

Decreasing or inhibiting the interaction between a viral protein and a host protein can

10   decrease or inhibit viral infection. Methods that can be used to decrease an interaction between a viral protein and one or more host proteins (such as at least 2 host proteins, or at least 3 host proteins), include but are not limited to, disrupting expression of a host nucleic acid sequence encoding the host protein, (for example by functionally deleting the coding sequence, such as by a mutation, insertion, or deletion), altering the amino acid sequence or overall shape of the host protein,

15   degrading the host protein, employing an agent that interferes with the viral protein or host protein (such as a specific binding agent, for example an antibody or small molecule), or a combination thereof.

For example, expression of a host protein can occur during transcription or translation of a nucleic acid encoding the host protein, or as a result of post-translational modification of a host

20   protein. Methods that can be used to interrupt or alter transcription of a nucleic acid include, but are not limited to, site-directed mutagenesis, including mutations caused by a transposon or an insertional vector; and providing a DNA-binding protein that binds to the coding region of the host protein, thus blocking or interfering with RNA polymerase or another protein involved in transcription. Various inactive and recombinant DNA-binding proteins, and their effects on transcription, are discussed in

25   Lewin, *Genes VII*. Methods that can be used to interrupt or alter translation of a nucleic acid include, but are not limited to, using an antisense RNA or an siRNA that binds to a messenger RNA transcribed by the nucleic acid encoding the host polypeptide as described herein.

For example, exemplary host T-cell receptor polypeptides are encoded by target sequences associated with SEQ ID NOS: 1-20. Disrupting the expression of a nucleic acid including any target

30   sequence associated with SEQ ID NOS: 1-20 can reduce or prevent production of the corresponding T-cell receptor polypeptide, and without access to the T-cell receptor polypeptide, an HIV virus cannot infect the host cell. Even if expression of the host nucleic acid is not completely blocked or disrupted, virus infection can still be inhibited. For example, interference with a host protein encoded by any target sequence associated with SEQ ID NOS: 1-20 reduces the number of T-cell receptors

35   within that host cell available for recognition by an HIV virus, thus inhibiting HIV infection.

It is shown herein that inhibiting the interaction or activity between host Rab9 and HIV and Ebola using Rab9 siRNA molecules decreases infection of a host cell by the virus compared to the amount of infection in the absence of the siRNA molecules.

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Host proteins involved in viral infection, such as those encoded by target cDNA sequences associated with SEQ ID NOS: 1-227, 229, and 231, as well as target sequences associated with SEQ ID NOS: 228, 230, and 232, can be used to generate specific binding agents to those proteins. The specific binding agent can be an anti-protein binding agent, such as a monoclonal or polyclonal

5.   antibody. Anti-protein binding agents can provide a prophylactic or therapeutic effect, for example by interfering with viral infection. Assays to determine whether an antibody interferes with viral infection are described herein. Antibodies that recognize a host protein involved in viral infection can prevent a virus or portion thereof (such as a viral protein) from binding to a host protein involved in viral infection. For example, a monoclonal or polyclonal antibody that binds to a V beta T-cell

10   receptor on a cell can block the binding of HIV to that T-cell receptor, thus blocking infection of that cell. Effective amounts of such specific binding agents can be administered alone to a subject, or as part of a pharmaceutical composition, for the treatment of viral infection or as a prophylactic measure prior to the time the subject is exposed to the virus. In another example, specific binding agents that recognize a host protein involved in viral infection, such as β-chimerin or Rab9, can be used can be

15   used to screen for the presence of the host protein, in other cells, tissues or lysates, including a biological sample obtained from a subject.

Host nucleic acids and polypeptides described herein, such as target sequences associated with SEQ ID NOS: 1-232, can be used for prophylactic or therapeutic uses. For example, polypeptides with structures mimicking a protein recognized by a virus can be administered to a

20   subject as a pharmaceutical composition. These polypeptides interact with a virus already infecting that subject, or provide a prophylactic defense mechanism against infection if the subject is at risk of exposure to a virus. For example, polypeptides structurally similar to the T-cell receptor V beta 2.1 chain are recognized by HIV. If such polypeptides are administered to an HIV-positive subject, the viruses already present in the subject interact with those polypeptides in addition to that subject's T-

25   cell receptors, thus inhibiting the rate at which HIV infects T-cells. The administered polypeptides act as "decoys" to block HIV from interacting with T-cell receptors. As another example, an agent that otherwise interferes with the interaction between a virus and a host protein can provide a similar prophylactic effect. For example, a chemical compound or anti-AMT binding agent (such as an antibody) that interferes with the interaction between AMT and an influenza virus (including an

30   enzymatic inhibitor of AMT) provides a prophylactic or therapeutic effect against influenza A infection when provided to a host cell or administered to a host subject.

Additionally, the proteins described herein can be used to screen samples for the presence or absence of a particular antibody. For example, a β-chimerin or Rab9 protein can be used in an ELISA to screen a sample obtained from an individual for the presence of anti-β-chimerin or anti-

35   Rab9 antibodies generated by that individual, such as a blood sample.

Using a method similar to that described for nucleic acid binding agents above, protein binding agents (such as agents that specifically bind β-chimerin, Rab9, or V beta T-cell receptor proteins) can be used to screen cells, individuals or populations for the presence or absence of

polypeptides related to infection (such as HIV, Ebola, or influenza infection), thus providing
information about the susceptibility or resistance of that individual or population to viral infection.

The host nucleic acids, proteins, and related specific binding agents described herein can be
used as models for the design of anti-viral drugs. For example, the three-dimensional structure of a
5   protein described herein, such as β-chimerin, can be used in computer modeling of chemotherapeutic
agents that block the activity of that moiety, for example by binding the protein. As another example,
a monoclonal antibody can be used in a competitive binding assay to screen for other compounds that
bind the same antigen.

10   Screening for Resistance to Infection
Also provided herein are methods of screening host subjects for resistance to infection by
characterizing a nucleotide sequence of a host nucleic acid or the amino acid sequence of a host
polypeptide (such as those shown in Table 1, or any target sequence associated with SEQ ID NOS: 1-
232).

15   For example, the T-cell receptor V beta 2.1 chain nucleic acid of a subject can be isolated,
sequenced, and compared to SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20).
The greater the similarity between that subject's V beta 2.1 chain nucleic acid and the sequence
shown in SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO: 20), the more
susceptible that person is to HIV infection, while a decrease in similarity between that subject's V
20   beta 2.1 chain nucleic acid and SEQ ID NO: 20 (or a target sequence associated with SEQ ID NO:
20), the more resistant that subject can be to HIV infection.

In another example, the aminomethyltransferase (AMT) nucleic acid of a subject can be
isolated, sequenced, and compared to SEQ ID NOS: 36-37 (or a target sequence associated with SEQ
ID NOS: 36-37). The greater the similarity between that subject's AMT nucleic acid and the
25   sequence shown in SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37),
the more susceptible that person is to influenza A infection, while a decrease in similarity between
that subject's AMT nucleic acid and SEQ ID NOS: 36-37 (or a target sequence associated with SEQ
ID NOS: 36-37), the more resistant that subject can be to influenza A infection.

In yet another example, the Ras oncogene family member Rab9 nucleic acid of a subject can
30   be isolated, sequenced, and compared to SEQ ID NOS: 118-119 (or a target sequence associated with
SEQ ID NOS: 118-119). The greater the similarity between that subject's Rab9 nucleic acid and the
sequence shown in SEQ ID NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-
119), the more susceptible that person is to infection by a pathogen that uses lipid rafts, such as those
listed in Table 2, while a decrease in similarity between that subject's Rab9 nucleic acid and SEQ ID
35   NOS: 118-119 (or a target sequence associated with SEQ ID NOS: 118-119), the more resistant that
subject may be to infection by a pathogen that uses lipid rafts.

Assessing the genetic characteristics of a population can provide information about the
susceptibility or resistance of that population to viral infection. For example, polymorphic analysis of
AMT alleles in a particular human population, such as the population of a particular city or

geographic area, can indicate how susceptible that population is to influenza A infection. A higher percentage of AMT alleles substantially similar to SEQ ID NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37) indicates that the population is more susceptible to influenza A infection, while a large number of polymorphic alleles that are substantially different than SEQ ID

5   NOS: 36-37 (or a target sequence associated with SEQ ID NOS: 36-37) indicates that a population is more resistant to influenza A infection. Such information can be used, for example, in making public health decisions about vaccinating susceptible populations.

Transgenic Cells and Non-Human Mammals

10   Transgenic animal models, including recombinant and knock-out animals, can be generated from the host nucleic acids described herein. Exemplary transgenic non-human mammals include, but are not limited to, mice, rats, chickens, cows, and pigs. In certain examples, a transgenic non-human mammal has a knock-out of one or more of the target sequences associated with SEQ ID NOS: 1-35, and has a decreased viral susceptibility, for example infection by HIV. In certain

15   embodiments, a transgenic non-human mammal has a knock-out of any of the target sequences associated with SEQ ID NOS: 36-63, and has a decreased viral susceptibility, for example infection by influenza A. In certain examples, a transgenic non-human mammal has a knock-out of any of the target sequences associated with SEQ ID NOS: 64-232, and has a decreased viral susceptibility, for example infection by Ebola. In certain examples, a transgenic non-human mammal has a knock-out

20   of any target sequence associated with SEQ ID NOS: 118-119, and has a decreased susceptibility to infection by a pathogen that uses a lipid raft, such as those listed in Table 2. Such knock-out animals are useful for reducing the transmission of viruses from animals to humans. In addition, animal viruses that utilize the same targets provided herein can be decreased in the animals.

        Expression of the sequence used to knock-out or functionally delete the desired gene can be
25   regulated by chosing the appropriate promoter sequence. For example, constitutive promoters can be used to ensure that the functionally deleted gene is never expressed by the animal. In contrast, an inducible promoter can be used to control when the transgenic animal does or does not express the gene of interest. Exemplary inducible promoters include tissue-specific promoters and promoters responsive or unresponsive to a particular stimulus (such as light, oxygen, chemical concentration,

30   such as a tetracycline inducible promoter).

        For example, a transgenic mouse including an AMT gene (such as a target sequence associated with SEQ ID NOS: 36-37), or a mouse having a disrupted AMT gene, can be examined during exposure to various mammalian viruses related to influenza A. Comparison data can provide insight into the life cycles of influenza and related viruses. Moreover, knock-out animals (such as

35   pigs) that are otherwise susceptible to an infection (for example influenza) can be made to determine the resistance to infection conferred by disruption of the gene.

        Transgenic pigs having a disrupted human protein tyrosine phosphatase gene can be produced and used as an animal model to determine other types of infections, including viral infections in mammals related to influenza A. A transgenic pig resistant to infection by viruses other

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than influenza A is used to demonstrate the relatedness of influenza and those other viruses. Transgenic animals, including methods of making and using transgenic animals, are described in various patents and publication, such as WO 01/43540; WO 02/19811; U.S. Pub. Nos: 2001-0044937 and 2002-0066117; and U.S. Pat. Nos: 5,859,308; 6,281,408; and 6,376,743; and the references cited

5   therein.

Cells including an altered or disrupted host nucleic acid or polypeptide having a role in viral infection (such as a target sequence associated with SEQ ID NOS: 1-232), are resistant to infection by a virus (see Example 2). Such cells may therefore include cells having decreased susceptibility to HIV infection (such as cells having altered or disrupted target sequence associated with SEQ ID

10   NOS: 1-35), Ebola infection (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 64-232), or influenza A (such as cells having altered or disrupted target sequence associated with SEQ ID NOS: 36-63). For example, cells in which a β-chimerin gene was disrupted using the gene-trap method remain CD4+ after HIV infection and do not produce further detectable HIV virus particles. Thus, disrupting the expression of β-chimerin can confer resistance on the cell to

15   infection by HIV. Additionally, interfering with the activity of β-chimerin, such as contacting a β-chimerin with an enzymatic inhibitor or an anti-β-chimerin binding agent, can confer a similar resistance to HIV infection.

Screening for Agents that Decrease Viral Infection

20   A host nucleic acid or polypeptide involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, and peptides listed in Table 1, can be used to identify agents that inhibit the binding of a virus or viral protein to a host nucleic acid, a host protein, or another target protein capable of binding to the virus or viral protein. In some examples, a host molecule, such as a host protein or nucleic acid is contacted with a viral molecule, such as a virus or portion

25   thereof, for example as a viral protein. One or more test agents are contacted with the host molecule, the viral molecule, both both molecules, before, during or after contacting the host and viral molecules. Subsequently, it is determined whether binding of the viral molecule to the host molecule is decreased in the presence of the test agent, wherein a decrease in binding is an indication that the test agent decreases the binding of viral protein to the target protein.

30   In other examples, a cell-based assay is used to identify proteins that decrease viral infection, for example using the yeast two-hybrid system.

For example, the binding of the T-cell receptor V-D-J beta 2.1 chain polypeptide to HIV (or an HIV envelope glycoprotein) can be determined in the presence of a test agent. A decrease in binding activity between the T-cell receptor V-D-J beta 2.1 chain polypeptide and HIV indicates that

35   the test agent decreases the binding of HIV to the T-cell receptor V-D-J beta 2.1 chain, and the agent is a candidate for use as an anti-HIV agent. A decrease in binding activity can be determined by a comparison to a reference standard, such as a binding activity reported in the scientific literature, or to a control. Any suitable compound or composition can be used as a test agent, such as organic or inorganic chemicals, including aromatics, fatty acids, and carbohydrates; peptides, including

59

monoclonal antibodies, polyclonal antibodies, and other specific binding agents; or nucleic acids.
The virus or viral molecule can be obtained from any suitable virus, such as HIV, influenza A, Ebola,
and related viruses.

Therapeutic agents identified with the disclosed approaches can be used as lead compounds

5   to identify other agents having even greater antiviral activity. For example, chemical analogs of
identified chemical entities, or variant, fragments of fusions of peptide agents, are tested for their
ability to decrease viral infection using the disclosed assays. Candidate agents are also tested tested
for safety in animals and then used for clinical trials in animals or humans.

10   Microarrays

The host nucleic acids or proteins disclosed herein having a role in viral infection, such as a
target sequence associated with SEQ ID NOS: 1-232, can be used in an array. The array can be a
microarray, such as a nucleic acid array that includes probes to different polymorphic alleles of a
human AMT gene (for example target sequence associated with SEQ ID NOS: 36-37) or a human

15   Rab9 gene (for example target sequence associated with SEQ ID NOS: 118-119). Kits can be
generated, such as diagnostic kits or kits for screening for the presence or absence of a host nucleic
acid within a biological sample obtained from a subject or kits for administering an effective amount
of a specific binding agent to a subject for a therapeutic or prophylactic purpose.

20   The following examples are provided to illustrate particular features of certain embodiments,
but the scope of the claims should not be limited to those features exemplified.

                                        Example 1
                    Generation of Cells with Increased Resistance to Viral Infection

25   The gene-trap method was used to identify cellular genes needed for viral propagation but
whose inactivation is not lethal to the host cell. This was accomplished by using a Moloney murine
leukemia virus-derived shuttle vector that encodes for a promoterless neomycin-resistance gene (FIG.
1). This vector integrates into the host genome at transcriptionally active genes, thereby disrupting
the host gene but utilizing the host promoter to drive neomycin resistance carried by the vector. The

30   cells are then infected with the desired virus. Cells surviving the viral infection carry an interrupted
host gene that is needed during the viral life cycle. Since the construct is a shuttle vector, it can
function as a plasmid and can be moved from mammalian to bacterial systems, facilitating subcloning
and DNA sequencing. Using this approach, loci involved in, and in some cases required for viral
infection, for example by HIV-1 and HIV-2, influenza A and Ebola virus were identified.

35

Tissue culture

Sup-T1 human lymphoblastic leukemia cells were cultured in RPMI-1640 medium
supplemented with 10% heat-inactivated fetal calf serum (FCS), penicillin, streptomycin and
Fungisome. MDCK normal canine kidney cells were cultured in DMEM supplemented with 10%

60

fetal bovine serum (FBS), penicillin, streptomycin. Vero African green monkey kidney cells were cultured in DMEM supplemented with 10% FBS, amphotericin B, streptomycin, and Glutamine. All cultures were grown under 5% CO_2. Selection by all media was done in the presence of either 1 mg/ml (Sup-T1 and MDCK cells) or 400 mg/ml G418 (Geneticin; Vero cells).

5

Generation of gene-trapped library of cells

Parental, virus sensitive cells were plated and infected with U3neoSV1 as follows. Retrovirus vectors were obtained from H. Earl Ruley (Department of Microbiology and Immunology, Vanderbilt University School of Medicine, Nashville, TN). Stocks of the U3neoSV1 virus were

10   prepared as described (Chen et al., Gene trap retroviruses in Methods in Molecular Genetics (1994), page 123, herein incorporated by reference).

FIG. 1 illustrates the U3neoSV1 retroviral vector, which contains a promoterless neomycin phosphotransferase gene (Neo^R) within the U3 unique sequence of the 5' long terminal repeat (LTR) of MMLV. Additionally, a second mutationally inactivated copy of neo is present in the 3' LTR.

15   Portions of the MMLV genome were removed to impair replication, and were replaced with the β-lactamase gene which confers ampicillin resistance (Amp^R) to E. coli as well as an E. coli origin of replication (ori), flanked by two unique restriction sites for BamHI (position 2570) and EcoRI (position 4175). Sites and orientations of primers used for sequence analysis of cloned genomic fragments are indicated by the triangular arrowheads.

20   Parental, virus sensitive cells (106 Sup-T1 for HIV, Madin-Darby canine kidney, (MDCK) for influenza A, or Vero cells for Ebola) were plated for 12 hours before infection, after which U3neoSV1 was added at a multiplicity of infection (MOI) of 0.1, as titered by adding 1 ml of diluted stocks to cultured cells in the presence of 4 µg/ml polybrene. The cells were incubated at 37°C for one hour, 10 ml of fresh medium added, and the cells were incubated overnight at 37°C. The next

25   day, the medium was replaced with the appropriate media containing 1 mg/ml G418 and maintained until surviving cells approached confluence, which was usually about two weeks.

Upon random integration of the U3neoSV1 vector into the host genome, endogenous promoters result in expression of Neo^R, while expression of the exons 3' to the site of integration is disrupted. Therefore, only those events occurring at transcriptionally active promoters of non-

30   essential genes are selected.

A pool of the surviving cells, termed a library, including many cells bearing different disrupted genes was then exposed to the pathogen of interest. The resulting Sup-T1 library cells, MDCK library cells, and Vero library cells were infected HIV-1 and HIV-2; the A/PR/8/34 virus reassortant having A/Johannesburg/82/96 glycoproteins (H1N1); and Ebola, respectively, as follows.

35   An aliquot of the cell library was infected with three rounds of HIV-1 and three rounds of HIV-2 (3Bx in BC7 cells), normally a lethal event for Sup T-1 cells (FIG. 4). Approximately 3 x 10^8 actively growing Sup-T1 library cells were infected with the CXCR4 cytopathic HIV-1 strain LAI at an MOI of 10, approximately 100 fold greater that that normally used for spreading infection in culture. The cells were incubated with the virus for four hours in 2 ml of medium, then grown in bulk

at 10^6 cells/ml for two weeks, at which time G418 was added to a final concentration of 1 mg/ml and the cultures continued for an additional two weeks. The surviving cells were exposed to two further rounds of HIV-1 infection as described above and shown in FIG. 4.

5   Following HIV-1 infection, surviving cells were incubated 1:100 with BC7 T cells constitutively expressing the HIV-2 strain 3BX, which was modified to infect regardless of CD4 status, solely using the CXCR4 receptor. Cells were coincubated for two weeks followed by selection with 1 mg/ml G418 (same as FIG. 4, but with HIV-2 instead of HIV-1). The surviving cells were exposed to two further rounds of HIV-2 infection.

The final cell culture was selected using anti-CD4 magnetic microbeads (Miltyni) and
10   divided into 2.0 ml cultures containing 1000 cells each. These were then infected with LAI at an MOI of 10. Surviving cells from each culture were subjected to limit dilution, or growth on methylcellulose, and expanded in selection medium. The isolated clones were identified as being CD4 and CXCR4 positive following flow cytometry analysis using standard protocols. Several cell isolates were resistant to further HIV infection with unique expression of CD4 cell surface antigen.

15   For influenza infection, approximately 10^7 actively growing MDCK library cells were washed with phosphate buffered saline (Gibco) and infected with the A/PR/8/34 virus reassortant having A/Johannesburg/82/96 glycoproteins (H1N1) at an MOI of 20-30 in 250 µl DMEM in a T-25 flask. The cells were incubated with the virus for two hours, and the inoculum was subsequently replaced with DMEM, supplemented with 2% FBS and 1 µg/ml TPCK trypsin (to cleavage-activate
20   HA of new progeny virus). The cells were incubated for 18 hours to provide 2-3 rounds of infection. The maintenance medium was removed and replaced with selection medium (DMEM with 10% FBS and 1 mg/ml neomycin) and survivors allowed to expand. The surviving cells were exposed to one additional round of infection as described.

For filovirus infection, vero library cells were infected with either the Gulu 2000 or Zaire
25   1976 Ebola (EBO) strains, or the Voege 1967 strain of Marburg (MBG) at an MOI of greater than one in T-75 flasks in medium supplemented with 400 mg/ml G418. After a cytopathic effect (CPE) of 4+ was attained (greater than one week), survivors were harvested and reseeded undiluted and at 1:16 and 1:256 dilutions in selection medium. Wells with growth after 10 or more days were reinoculated into T12.5 flasks in selection medium and allowed to expand.
30   Cells surviving Ebola or influenza infection were cloned by either limiting dilution or growth on methylcellulose. The isolates were characterized phenotypically by flow cytometry and the interrupted gene determined by inverse PCR, cloning into BAC, or by the use of the shuttle feature of the vector followed by DNA sequence analysis.

35   Example 2
                        Cloning and Sequencing of Trapped Genes
This example describes the methods used to clone the sequences conferring resistance to the library of cells surviving viral infection. The identified sequences (SEQ ID NOS: 1-227, 229, 231)

encode host proteins that are involved in pathogen infection, and in some cases are required for the infectivity by the pathogen.

Isolation of trapped genes

5   The genomic DNA from actively growing virus-resistant isolates was extracted, prepared, and electroporated into cells as follows. Cellular DNA from actively growing virus-resistant isolates was extracted from one million cells using the QIAamp DNA Blood Mini Kit (Qiagen, Inc.) according to the manufacturer's instructions. Genomic DNA was digested at a final concentration of 150 µg/ml with either EcoRI or BamHI (New England Biolabs) at 1.5 or 2 units/µl, respectively (see

10   FIG. 1). Digested DNA was ethanol precipitated using oyster glycogen (Sigma) as a carrier, resuspended to a final concentration of 60 ng/µl and ligated using T4 DNA ligase (New England Biolabs). Genomic digestion resulted in the fragmentation of the retrovirus and the genomic DNA. Ligations were subsequently ethanol precipitated in the presence of glycogen, resuspended in 3 µl water and used directly to transform E. coli.

15   A 1.5 µl aliquot of each precipitated ligation was added to thawed Genehog cells (Invitrogen) or SURE cells (Stratagene), electroporated using a GenePulser (BioRad) according to the manufacturer's instructions, and plated onto Luria broth (LB) agar (1% tryptone, 0.5% yeast extract, 0.5% NaCl, 2% agar) containing 100 µg/µl carbenicillin (Sigma). Clones were isolated after 24 hours and used to inoculate 3 ml LB containing 100 µg/µl carbenicillin. Plasmid DNA was prepared after

20   overnight growth using the QIAprep Spin Miniprep Kit (QIAGEN, Inc.) according to the manufacturer's instructions and eluted in water.

Sequencing of Shuttle Clones

Due to the position of the unique sites in U3neoSV1, BamHI digestion facilitates cloning of

25   DNA 3' to the site of integration, while EcoRI digestion results in the cloning of genomic DNA 5' to the site of integration. Using oligonucleotides homologous to the U3neoSV1 fragment, the sequence of the disrupted genomic DNA flanking the gene-trap insertion site was determined as follows.

Sequencing reactions were performed using the ABI BigDye terminator cycle sequencing kit with reaction products resolved on either an ABI 3100 Genetic Analyzer or an ABI 377 DNA

30   Sequencer (Applied Biosystems, Foster City, CA). Sequences were obtained by using oligonucleotides 5'-ATCTTGTTCAATCATGCG (SEQ ID NO: 235) and 5'-GGGTCTGACGCTCATG (SEQ ID NO: 236) for EcoRI-generated shuttle clones, or 5'-GATAGGTGCCTCACTG (SEQ ID NO: 237) for BamHI-generated shuttle clones.

35   ### Sequence analysis

Sequences obtained from shuttle clones were analyzed by the Repeatmasker Web Server, available on the Internet at the website for the Department of Molecular Biotechnology, University of Washington, followed by standard nucleotide-nucleotide BLAST (blastn) against the National Center for Biotechnology Information databases, including nr (non-redundant

63

GenBank+EMBL+DDBJ+PDB sequences), est (expressed sequence tags) and htgs (unfinished High
Throughput Genomic Sequences: phases 0, 1 and 2). Additionally, a nucleotide-protein database
(blastx) analysis was performed against the nr database.

5   *Candidate Host Genes Required for Pathogenesis*

             Candidate host genes required for the indicated pathogen, which were cloned via the gene-
      trap method and sequenced, are presented in Table 1 and in SEQ ID NOS: 1-226. The CD4$^+$, latently
      infected, noninfectious HIV-resistant isolates 18B, 18E, 2B, and 2E were used to recover the genes
      involved in HIV-1 and HIV-2 pathogenesis, influenza A-resistant isolates B1, B3, B5, B6, and B7
10   were use to recover the host genes involved in influenza A pathogenesis, and Ebola-resistant isolates
      ZV and MV were used to recover the host genes involved in Ebola pathogenesis. Candidate genes
      can be validated by siRNA and cDNA complementation, as described in Example 3.

             In summary, using the U3neoSV1 gene-trap, sixteen HIV-1 and -2 resistant Sup-T1 cell
      lines, and fifteen influenza A resistant MDCK cell lines were isolated and characterized. Twenty-
15   three EBO-Zaire resistant Vero cell line pools, twenty-four EBO-Gulu resistant pools, and thirty
      MBG resistant pools were screened. The shuttle-vector design of the U3neoSV1 gene-trap allowed
      identification of multiple host genes involved in the pathogenesis of HIV-1, HIV-2, influenza A, and
      Ebola, which are described herein and summarized in Table 1 and sequences provided in SEQ ID
      NOS: 1-232. Cross-resistance of resistant isolates to multiple pathogens can be quickly examined to
20   reveal common pathways in the viral life cycles.

                                          Example 3
                         siRNA Molecules Decrease Viral Infection

             This example describes methods used to express siRNAs that recognize Rab9 (such as a
25   target sequence associated with SEQ ID NOS: 118-119), AXL (AXL receptor tyrosine kinase; such
      as a target sequence associated with SEQ ID NO: 226), CHN (beta-chimerin; such as a target
      sequence associated with SEQ ID NOS: 21-22), KOX (such as a target sequence associated with SEQ
      ID NO: 30), RBB (retinoblastoma binding protein 1; such as a target sequence associated with SEQ
      ID NOS: 120-122), KIAA1259; F3 (such as a target sequence associated with SEQ ID NO: 29), and
30   Mselb (mammalian selenium binding protein; such as a target sequence associated with SEQ ID NO:
      124).

             The following Rab9 siRNA sequences were generated by Dharmacon, RNA Technologies
      (Lafayette, CO) using chemical synthesis: GGGAAGAGTTCACTTATGA (SEQ ID NO: 238);
      TCACAAAGCTTCCAGAACT (SEQ ID NO: 239); GTAACAAGATTGACATAAG (SEQ ID NO:
35   240); and GGAAGTGGATGGACATTTT (SEQ ID NO: 241).

             The following AXL (AXL receptor tyrosine kinase) siRNA sequences were generated by
      Dharmacon, RNA Technologies using chemical synthesis: GGUCAGAGCUGGAGGAUUU (SEQ
      ID NO: 242); GAAAGAAGGAGACCCGUUA (SEQ ID NO: 243);

64

CCAAGAAGAUCUACAAUGG (SEQ ID NO: 244); and GGAACUGCAUGCUGAAUGA (SEQ
ID NO: 245).

     siRNA sequences were also used that recognized CHN (beta-chimerin); KOX (similar to
KOX4 (LOC131880) and LOC166140); RBB (retinoblastoma binding protein 1); KIAA1259; F3 and

5   mammalian selenium binding protein. One skilled in the art will understand that siRNA sequences
that recognize other sequences involved in viral infection (such as a target sequence associated with
any of SEQ ID NOS: 1-232) can be desiged and prepared by commercial entities, such as
Dharmacon, RNA Technologies.

     The four siRNA sequences for each gene (CHN, KOX, RBB, RAB, KIAA1259, F3, ASL

10   and Mselb) were separately pooled. Each of the eight pools of siRNAs, hybridized to its appropriate
complement sequence, were used to transfect JC53 (HeLa cells modified to accept HIV), Vero
(monkey kidney cells), MDCK (dog kidney cells), or HEK (human kidney cells). All cells were
obtained from American Type Culture Collection (ATCC, Mannassas, VA). GFP siRNA sequences
were used as a negative control.

15   Cells (20,000 to 250,000) were incubated in serum free media for 24 hours. Cocktails were
made by mixing the appropriate duplex siRNAs (50-100 pmoles) with lipofectamine 2000 (4-16 µl)
and RNAse Inhibitor (1-4 µl) in a solution of Optimem (serum free medium) in a total volume of
200-2000 µl. The lipofectamine was allowed to incubate at room temperature for 5 minutes before
the addition of siRNA. Aliquots (50-500 µl) of the cocktail were added to the cells which were

20   incubated at 37°C for 48 hours. The cells were then infected with HIV, Ebola, or influenza and the
incubation continued for 3-7 days. Following transfection, several assays were conducted to confirm
transfection efficiency, and to determine the resistance of the cells to infection by various agents.

     Quantitation of p24 levels in HIV infected JC53 cells was determined using the Coulter
HIV-1 p24 Antigen Neutralization Kit according to the manufacturers recommendation. As shown in

25   FIG. 5, Rab9 siRNAs and mammalian selenium binding protein siRNAs each decreased HIV
infection by about 50% on day 4 post infection (day 7 post addition of siRNA). In addition, HIV
infection decreased by about 80-90% in the presence of beta-chimerin siRNAs, KOX (similar to
KOX4 (LOC131880) and LOC166140) siRNAs, or retinoblastoma binding protein 1 siRNAs.
However, HIV infection did not decrease in the presence of siRNAs that recognize KIAA1259, tissue

30   factor 3, or AXL receptor tyrosine kinase. It is possible that apoptosis is interrupted by the siRNAs,
so the cell lives through the infection but still makes virus. It is also possible that the p24 levels are
elevated but is not associated with infectious particles.

     To determine the level of Ebola infection in HEK293 cells transfected with Rab9 or AXL
siRNA, the presence of gp1 antigen was determined by using a fluorescent antibody to gp1 envelope

35   protein. Infection by Ebola decreased by at least about 90-95% in the presence of Rab9 siRNA, as
compared to the amount of infection in the absence of Rab9 siRNA. Infection by Ebola decreased by
at least about 80% in the presence of AXL siRNA, as compared to the amount of infection in the
absence of AXL siRNA.

Example 4

Expression of Rab9 siRNA Decreases Lipid Raft Formation

As described in Example 3, siRNA molecules that recognize Rab9 decrease viral infection. Rab9 transports late endosomes to trans-golgi. Based on these results, a model is proposed whereby Rab9 plays a role in lipid raft formation (FIG. 6). Lipid rafts are liquid-ordered microdomains enriched in sphingolipds and cholesterol, and are involved in biosynthetic traffic, signal transduction, and endocytosis. Viruses take advantage of ("hijack") rafts for completion of some steps of their replication cycle, such as entry into their cell host, assembly, and budding. Without wishing to be bound to a particular theory, it is proposed that Rab9 trafficks cholesterol, the dynamic glue that holds lipid rafts together. Further evidence for this hypothesis is based on observations of Neimann-Pick type C disease cells. Neimann-Pick type C is a genetic disease that results in accumulation of abnormally high levels of intracellular cholesterol. However, over expression of Rab9 in Neimann-Pick type C disease cells, decreases the level of cholesterol.

Examples of pathogens that hijack lipid rafts include, but are not limited to those shown in Table 2. In the absence of functional Rab9 and lipid rafts (or a decrease in the number of rafts), viruses may not be able to bud or be infectious. Therefore, the use of agents that decrease or inhibit Rab9 expression or activity can be used to decrease infection by other pathogens, as well as toxins such as anthrax, that hijack lipid rafts, such as those shown in Table 2.

Table 2: Pathogens that hijack lipid rafts.

Bacteria		Viruses	Protozoa
Intracellular survival	Toxin binding/oligomerization		
Campylobacter jujuni	*Vibrio cholerae*	SV40	*Toxoplasma gondii*
Legionella pneumophila	*Aeromonas hydrophilia*	Echovirus 1 and 11	*Plasmodium falciparum*
Brucella spp	*Clostridium spp.*	Avian sarcoma and leukosis virus	
FimH and Dr Escherichia coli	*Streptcoccus pyogenes*	Semiliki forest virus	
Salmonella typhimurium	*Bacillus anthracis*	Ecotropic mouse leukaemia virus	
Shigella flexneri	*Bacillus thuringiensis*	HTLV-1	
Chlamydia spp.	*Helicobacter pylori*	HIV-1	
Mycobacterium spp.	*Lysteria monocytogenes*	Ebola and Marburg viruses	
		Measles virus	
		Herpes Simplex virus	
		Influenza virus	
		Epstein-Barr virus	

This example therefore illustrates that identification of an agent (such as a small molecule or siRNA) that inhibits a particular pathogen can be used to inhibit other pathogens that have a similar mechanism of action.

66

Example 5

RNAi Molecules

This example describes methods that can be used to decrease or inhibit expression of any of
the genes listed in Table 1, or target sequences associated with SEQ ID NOS: 1-232, to decrease viral
infection, such as infection by HIV, Ebola, or influenza. Exemplary RNAi compounds are provided
for several different genes, such as beta-chimerin receptor tyrosine kinase, retinoblastoma binding
protein 1, *Homo sapiens* chromosome 10 open reading frame 3, *Homo sapiens* fer-1-like 3, myoferlin
(*C. elegans*), transcript variant 1, *Homo sapiens* chromosome 10 open reading frame 3 (C10orf3),
malic enzyme, cadherin related 23, sideroflexin 5, polybromo 1, elongation factor for selenoprotein
translation, integrin, beta 1, huntingtin interacting protein 1 and cyclin M2.

One skilled in the art will understand that RNAi molecules can be generated to any of the
genes listed in Table 1. Although only 27mers are shown in SEQ ID NOS: 246-845, this disclosure
is not limited to RNAi compounds of a particular length. An RNAi molecule can be any length, such
as at least about about 25 nucleotides, or even as many as 400 nucleotides. One skilled in the art will
also understand that RNAi sequences that recognize other sequences involved in viral infection (such
as a target sequence associated with any of SEQ ID NOS: 1-232) can be desiged and prepared by
commercial entities, such as Sequitur, Inc. (Natick, MA).

Using the methods described in Example 3, the disclosed RNAi compounds are used to
decrease viral infection. For example, a 27mer RNAi compound shown in any of SEQ ID NOS: 246-
845 is incubated with its reverse complement, allowing hybridization of the two molecules. In
particular examples, two or more, such as three or more, 27mer RNAi compounds are transfected into
a cell. This duplex molecule is contacted with a cell, such as a cell of a subject in whom decreased
viral infection is desired, under conditions that allow the duplex to enter the cell.

Example 6

Disruption of Gene Expression

This example describes methods that can be used to disrupt expression of a host gene, such
as those shown in Table 1 and target sequences associated with SEQ ID NOS: 1-232, and thereby
decrease activity of the proteins encoded by these sequences. Such methods are useful when it is
desired to decrease or inhibit viral infection. In a particular example, disrupted expression of at least
one target sequence associated with SEQ ID NOS: 1-232 in a host cell is used to treat a subject
having a viral infection, or susceptible to a viral infection. Methods useful for disrupting gene
function or expression are the use of antisense oligonucleotides, siRNA molecules (see Example 3),
RNAi molecules (see Example 5), ribozymes, and triple helix molecules. Techniques for the
production and use of such molecules are well known to those of skill in the art.

Antisense Methods

To design antisense oligonucleotides, a host mRNA sequence is examined. Regions of the sequence containing multiple repeats, such as TTTTTTTT, are not as desirable because they will lack specificity. Several different regions can be chosen. Of those, oligos are selected by the following characteristics: those having the best conformation in solution; those optimized for hybridization characteristics; and those having less potential to form secondary structures. Antisense molecules having a propensity to generate secondary structures are less desirable.

Plasmids including antisense sequences that recognize one or more of the target sequences associated with SEQ ID NOS: 1-232 (such as a sequence that encodes a protein listed in Table 1) can

10   be generated using standard methods. For example, cDNA fragments or variants coding for a host protein involved in viral infection are PCR amplified. The nucleotides are amplified using Pfu DNA polymerase (Stratagene) and cloned in antisense orientation a vector, such as pcDNA vectors (InVitrogen, Carlsbad, CA). The nucleotide sequence and orientation of the insert can be confirmed by sequencing using a Sequenase kit (Amersham Pharmacia Biotech).

Generally, the term "antisense" refers to a nucleic acid capable of hybridizing to a portion of

15   a host RNA sequence (such as mRNA) by virtue of some sequence complementarity. The antisense nucleic acids disclosed herein can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

Antisense nucleic acids are polynucleotides, and can be oligonucleotides (ranging from

20   about 6 to about 100 oligonucleotides). In one example, an antisense polynucleotide recognizes one or more of the target nucleic acid sequences associated with SEQ ID NOS: 1-227, 229, or 231. In specific examples, the oligonucleotide is at least 10, 15, or 100 nucleotides, or a polynucleotide of at least 200 nucleotides. However, antisense nucleic acids can be much longer. The nucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, and can include other appending

25   groups such as peptides, or agents facilitating transport across the cell membrane (Letsinger et al., Proc. Natl. Acad. Sci. USA 1989, 86:6553-6; Lemaitre et al., Proc. Natl. Acad. Sci. USA 1987, 84:648-52; WO 88/09810) or blood-brain barrier (WO 89/10134), hybridization triggered cleavage agents (Krol et al., BioTechniques 1988, 6:958-76) or intercalating agents (Zon, Pharm. Res. 5:539-49, 1988).

30   An antisense polynucleotide (including oligonucleotides) that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231, can be modified at any position on its structure with substituents generally known in the art. For example, a modified base moiety can be 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-

35   carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N-6-sopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-

oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-S-oxyacetic acid, 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, and 2,6-diaminopurine.

5   An antisense polynucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231, can include at least one modified sugar moiety such as arabinose, 2-fluoroarabinose, xylose, and hexose, or a modified component of the phosphate backbone, such as phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, or a formacetal or analog thereof.

10   In a particular example, an antisense polynucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 is an α-anomeric oligonucleotide. An α-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gautier *et al.*, *Nucl. Acids Res.* 15:6625-41, 1987). The oligonucleotide can be conjugated to another molecule, such as a

15   peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent. Oligonucleotides can include a targeting moiety that enhances uptake of the molecule by host cells. The targeting moiety can be a specific binding molecule, such as an antibody or fragment thereof that recognizes a molecule present on the surface of the host cell.

Polynucleotides disclosed herein can be synthesized by standard methods, for example by

20   use of an automated DNA synthesizer. As examples, phosphorothioate oligos can be synthesized by the method of Stein *et al.* (*Nucl. Acids Res.* 1998, 16:3209), methylphosphonate oligos can be prepared by use of controlled pore glass polymer supports (Sarin *et al.*, *Proc. Natl. Acad. Sci. USA* 85:7448-51, 1988). In a specific example, antisense oligonucleotide that recognizes one or more of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 includes catalytic RNA, or a

25   ribozyme (see WO 90/11364, Sarver *et al.*, *Science* 247:1222-5, 1990). In another example, the oligonucleotide is a 2'-0-methylribonucleotide (Inoue *et al.*, *Nucl. Acids Res.* 15:6131-48, 1987), or a chimeric RNA-DNA analogue (Inoue *et al.*, *FEBS Lett.* 215:327-30, 1987).

The antisense polynucleic acids disclosed herein include a sequence complementary to at least a portion of an RNA transcript of a gene, such as a target sequence associated with SEQ ID

30   NOS: 1-227, 229, or 231. However, absolute complementarity, although advantageous, is not required. A sequence can be complementary to at least a portion of an RNA, meaning a sequence having sufficient complementarily to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation can be assayed. The ability to hybridize depends on the degree of

35   complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The relative ability of polynucleotides (such as oligonucleotides) to bind to complementary strands is compared by determining the T_m of a hybridization complex of the poly/oligonucleotide and its complementary strand. The higher the T_m the greater the strength of the binding of the hybridized strands. As close to optimal fidelity of base pairing as possible achieves optimal

5   hybridization of a poly/oligonucleotide to its target RNA.

The amount of antisense nucleic acid that is effective in the treatment of a particular disease or condition (the therapeutically effective amount) depends on the nature of the disease or condition, and can be determined by standard clinical techniques. For example, it can be useful to use compositions to achieve sustained release of an antisense nucleic acid, for example an antisense

10   molecule that recognizes one or more target sequences associated with SEQ ID NOS: 1-227, 229, or 231. In another example, it may be desirable to utilize liposomes targeted via antibodies to specific cells.

As an alternative to antisense inhibitors, catalytic nucleic acid compounds, such as ribozymes or anti-sense conjugates, can be used to inhibit gene expression. Ribozymes can be

15   synthesized and administered to the subject, or can be encoded on an expression vector, from which the ribozyme is synthesized in the targeted cell (as in WO 9523225, and Beigelman *et al.* *Nucl. Acids Res.* 1995, 23:4434-42). Examples of oligonucleotides with catalytic activity are described in WO 9506764. Conjugates of antisense with a metal complex, such as terpyridylCu (II), capable of mediating mRNA hydrolysis, are described in Bashkin *et al.* (*Appl. Biochem Biotechnol.* 54:43-56,

20   1995).

Ribozymes

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme

25   molecule to complementary target RNA, followed by a endonucleolytic cleavage. Methods of using ribozymes to decrease or inhibit RNA expression are known in the art. An overview of ribozymes and methods of their use is provided in Kashani-Sabet (*J. Imvestig. Dermatol. Symp. Proc.*, 7:76-78, 2002).

Ribozyme molecules include one or more sequences complementary to the target host

30   mRNA and include the well-known catalytic sequence responsible for mRNA cleavage (see U.S. Pat. No. 5,093,246, herein incorporated by reference).

A ribozyme gene directed against any of the target sequences associated with SEQ ID NOS: 1-227, 229, or 231 can be delivered to a subject endogenously (where the ribozyme coding gene is transcribed intracellularly) or exogenously (where the ribozymes are introduced into a cell, for‑

35   example by transfection). Methods describing endogenous and exogenous delivery are provided in Marschall *et al.* (*Cell Mol. Neurobiol.* 14:523-38, 1994).

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites that include the following sequence: GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and ribonucleotides

70

corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features, such as secondary structure, that may render the oligonucleotide sequence unsuitable. The suitability of candidate targets may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection

5   assays.

For example, a plasmid that contains a riboyzme gene directed against a β-chimerin rho-GTPase, placed behind a promoter, can be transfected into the cells of a subject, for example a subject susceptible to HIV infection. Expression of this plasmid in a cell will decrease or inhibit β-chimerin rho-GTPase RNA expression in the cell. In another example, a plasmid that contains a

10   riboyzme gene directed against Rab9 placed behind a promoter, can be transfected into the cells of a subject, for example a subject susceptible to infection by a pathogen that utilizes lipid rafts, such as Ebola. Expression of this plasmid in a cell will decrease or inhibit Rab9 RNA expression in the cell. Other examples of using ribozymes to decrease or inhibit RNA expression can be found in WO 01/83754 (herein incorporated by reference).

15

Triple helix molecules

Nucleic acid molecules used in triplex helix formation should be single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is ideally designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable

20   stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC+ triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example,

25   contain a stretch of guanidine residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are

30   synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with one strand of a duplex first and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Example 7
Methods of Treatment

35   When the activity of a host cell protein or nucleic acid involved in viral infection is decreased by prematurely downregulating their levels of expressing using antisense molecules, a reduction in viral infection can be achieved. Antisense oligonucleotides, RNAi molecules, ribozymes, and siRNA molecules that recognize a host nucleic acid involved in viral infection

71

(Example 6) can therefore be used to disrupt cellular expression of a host protein involved in viral infection. The disclosed antisense, ribozyme, RNAi molecules and siRNA molecules can be administered to a subject alone, or in combination with other therapeutic agents such as anti-viral compounds.

5   A subject susceptible to or suffering from a viral infection, wherein decreased amounts of infection by the virus is desired, can be treated with a therapeutically effective amount of antisense, ribozyme, RNAi molecule or siRNA molecule (or combinations thereof) that recognizes a host sequence involved in viral infection, such as those shown in Table 1 or target sequences associated with SEQ ID NOS: 1-232. After the antisense, ribozyme, RNAi molecule or siRNA molecule has

10   produced an effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for diseases associated with viral infection.

          Similarly, other agents, such as an antibody that recognizes a host protein involved in viral infection and prevents the protein from interacting with a viral protein, can also be used to decrease

15   or inhibit viral infection. Other exemplary agents are those identified using the methods described in the Examples below. These agents, such as antibodies, peptides, nucleic acids, organic or inorganic compounds, can be can be administered to a subject in a therapeutically effective amount. After the agent has produced an effect (a decreased level of viral infection is observed, or symptoms associated with viral infection decrease), for example after 24-48 hours, the subject can be monitored for

20   diseases associated with viral infection.

          The treatments disclosed herein can also be used prophylactically, for example to inhibit or prevent a viral infection. Such administration is indicated where the treatment is shown to have utility for treatment or prevention of the disorder. The prophylactic use is indicated in conditions known or suspected of progressing to disorders associated with a viral infection.

25

Example 8
Recombinant Expression

          With the disclosed host sequences involved in viral infection, native and variant sequences can be generated. Expression and purification by standard laboratory techniques of any variant, such

30   as a polymorphism, mutant, fragment or fusion of a sequence involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, is enabled. One skilled in the art will understand that the sequences involved in viral infection, as well as variants thereof, can be produced recombinantly in any cell or organism of interest, and purified prior to use.

          Methods for producing recombinant proteins are well known in the art. Therefore, the scope

35   of this disclosure includes recombinant expression of any host protein or variant or fragment thereof involved in viral infection. For example, see U.S. Patent No: 5,342,764 to Johnson et al.; U.S. Patent No: 5,846,819 to Pausch et al.; U.S. Patent No: 5,876,969 to Fleer et al. and Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, New York, 1989, Ch. 17, herein incorporated by reference).

Briefly, partial, full-length, or variant cDNA sequences that encode for a protein involved in viral infection, such as a target sequence associated with SEQ ID NOS: 1-232, can be ligated into an expression vector, such as a bacterial expression vector. Proteins or peptides can be produced by placing a promoter upstream of the cDNA sequence. Examples of promoters include, but are not

5   limited to *lac*, *trp*, *tac*, *trc*, major operator and promoter regions of phage lambda, the control region of fd coat protein, the early and late promoters of SV40, promoters derived from polyoma, adenovirus, retrovirus, baculovirus and simian virus, the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, the promoter of the yeast alpha-mating factors and combinations thereof.

10   Vectors suitable for the production of intact proteins include pKC30 (Shimatake and Rosenberg, 1981, *Nature* 292:128), pKK177-3 (Amann and Brosius, 1985, *Gene* 40:183) and pET-3 (Studiar and Moffatt, 1986, *J. Mol. Biol.* 189:113). A DNA sequence can be transferred to other cloning vehicles, such as other plasmids, bacteriophages, cosmids, animal viruses and yeast artificial chromosomes (YACs) (Burke *et al.*, 1987, *Science* 236:806-12). These vectors can be introduced

15   into a variety of hosts including somatic cells, and simple or complex organisms, such as bacteria, fungi (Timberlake and Marshall, 1989, *Science* 244:1313-7), invertebrates, plants (Gasser and Fraley, 1989, *Science* 244:1293), and mammals (Pursel *et al.*, 1989, *Science* 244:1281-8), that are rendered transgenic by the introduction of the heterologous cDNA.

For expression in mammalian cells, a cDNA sequence, such as a coding sequence of any

20   target sequence associated with SEQ ID NOS: 1-227, 229, or 231, can be ligated to heterologous promoters, such as the simian virus SV40, promoter in the pSV2 vector (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072-6), and introduced into cells, such as monkey COS-1 cells (Gluzman, 1981, *Cell* 23:175-82), to achieve transient or long-term expression. The stable integration of the chimeric gene construct may be maintained in mammalian cells by biochemical

25   selection, such as neomycin (Southern and Berg, 1982, *J. Mol. Appl. Genet.* 1:327-41) and mycophoenolic acid (Mulligan and Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072-6).

The transfer of DNA into eukaryotic, such as human or other mammalian cells is a conventional technique. The vectors are introduced into the recipient cells as pure DNA (transfection) by, for example, precipitation with calcium phosphate (Graham and vander Eb, 1973,

30   *Virology* 52:466) strontium phosphate (Brash *et al.*, 1987, *Mol. Cell Biol.* 7:2013), electroporation (Neumann *et al.*, 1982, *EMBO J.* 1:841), lipofection (Felgner *et al.*, 1987, *Proc. Natl. Acad. Sci USA* 84:7413), DEAE dextran (McCuthan *et al.*, 1968, *J. Natl. Cancer Inst.* 41:351), microinjection (Mueller *et al.*, 1978, *Cell* 15:579), protoplast fusion (Schafner, 1980, *Proc. Natl. Acad. Sci. USA* 77:2163-7), or pellet guns (Klein *et al.*, 1987, *Nature* 327:70). Alternatively, the cDNA can be

35   introduced by infection with virus vectors, for example retroviruses (Bernstein *et al.*, 1985, *Gen. Engrg.* 7:235) such as adenoviruses (Ahmad *et al.*, *J. Virol.* 57:267, 1986) or Herpes (Spaete *et al.*, *Cell* 30:295, 1982).

Example 9

Pharmaceutical Compositions and Modes of Administration

Various delivery systems for administering the therapies disclosed herein are known, and include encapsulation in liposomes, microparticles, microcapsules, expression by recombinant cells, receptor-mediated endocytosis (Wu and Wu, *J. Biol. Chem.* 1987, 262:4429-32), and construction of therapeutic nucleic acids as part of a retroviral or other vector. Methods of introduction include, but are not limited to, topical, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, and oral routes. The compounds can be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (for example, oral mucosa, rectal, vaginal and intestinal mucosa, etc.) and can be administered

10   together with other biologically active agents. Administration can be systemic or local. Pharmaceutical compositions can be delivered locally to the area in need of treatment, for example by topical application.

Pharmaceutical compositions are disclosed that include a therapeutically effective amount of an RNA, DNA, antisense molecule, ribozyme, RNAi molecule, siRNA molecule, specific-binding

15   agent, or other therapeutic agent, alone or with a pharmaceutically acceptable carrier. Furthermore, the pharmaceutical compositions or methods of treatment can be administered in combination with (such as before, during, or following) other therapeutic treatments, such as other antiviral agents.

Delivery systems

20   The pharmaceutically acceptable carriers useful herein are conventional. *Remington's Pharmaceutical Sciences*, by Martin, Mack Publishing Co., Easton, PA, 15th Edition (1975), describes compositions and formulations suitable for pharmaceutical delivery of the therapeutic agents herein disclosed. In general, the nature of the carrier will depend on the mode of administration being employed. For instance, parenteral formulations usually include injectable

25   fluids that include pharmaceutically and physiologically acceptable fluids such as water, physiological saline, balanced salt solutions, aqueous dextrose, sesame oil, glycerol, ethanol, combinations thereof, or the like, as a vehicle. The carrier and composition can be sterile, and the formulation suits the mode of administration. In addition to biologically-neutral carriers, pharmaceutical compositions to be administered can contain minor amounts of non-toxic auxiliary

30   substances, such as wetting or emulsifying agents, preservatives, and pH buffering agents and the like, for example sodium acetate or sorbitan monolaurate.

The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. For solid compositions (for example powder, pill, tablet, or capsule forms), conventional non-toxic solid carriers can include, for example, pharmaceutical grades

35   of mannitol, lactose, starch, sodium saccharine, cellulose, magnesium carbonate, or magnesium stearate. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides.

Embodiments of the disclosure including medicaments can be prepared with conventional pharmaceutically acceptable carriers, adjuvants and counterions as would be known to those of skill in the art.

The amount of therapeutic agent effective in decreasing or inhibiting viral infection can
5   depend on the nature of the virus and its associated disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* assays can be employed to identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each subject's circumstances. Effective doses can be extrapolated
10   from dose-response curves derived from *in vitro* or animal model test systems.

The disclosure also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by
15   the agency of manufacture, use or sale for human administration. Instructions for use of the composition can also be included.

Administration of Nucleic Acids

In an example in which a nucleic acid is employed to reduce viral infection, such as an
20   antisense, RNAi molecule, or siRNA molecule, the nucleic acid can be delivered intracellularly (for example by expression from a nucleic acid vector or by receptor-mediated mechanisms), or by an appropriate nucleic acid expression vector which is administered so that it becomes intracellular, for example by use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (such as a gene gun; Biolistic, Dupont), or coating with lipids or cell-
25   surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (for example Joliot *et al.*, *Proc. Natl. Acad. Sci. USA* 1991, 88:1864-8). The present disclosure includes all forms of nucleic acid delivery, including synthetic oligos, naked DNA, plasmid and viral, integrated into the genome or not.

30   **Example 10**
                        in vitro Screening Assay for Agents that Decrease Viral Infection

This example describes *in vitro* methods that can be used to screen test agents for their ability to interfere with or even inhibit viral infection of a host cell. As disclosed in the Examples above, the disclosed host proteins (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232, as well as variants, fragments, and fusions thereof) are involved

5   in viral infection (such as infection by HIV, Ebola, and influenza A), and the host protein/viral protein interaction is a component in the ability of a virus to infect a cell. Therefore, screening assays can be used to identify and analyze agents that decrease or interfere with this interaction. For example, the following assays can be used to identify agents that interfere with the interaction of the disclosed host proteins (such as those listed in Table 1 and the target protein sequences associated

10   with SEQ ID NOS: 1-232) with a viral protein sequence. However, the present disclosure is not limited to the particular methods disclosed herein.

Agents identified via the disclosed assays can be useful, for example, in decreasing or even inhibiting viral infection by more than an amount of infection in the absence of the agent, such as a decrease of at least about 10%, at least about 20%, at least about 50%, or even at least about 90%.

15   This decrease in viral infection can serve to ameliorate symptoms associated with viral infection, such as fever. Assays for testing the effectiveness of the identified agents, are discussed below.

Exemplary test agents include, but are not limited to, any peptide or non-peptide composition in a purified or non-purified form, such as peptides made of D-and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam *et al.*, *Nature* 354:82-4,

20   1991), phosphopeptides (such as in the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang *et al.*, *Cell* 72:767-78, 1993), antibodies, and small or large organic or inorganic molecules. A test agent can also include a complex mixture or "cocktail" of molecules.

The basic principle of the assay systems used to identify agents that interfere with the

25   interaction between a host protein, such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232, and its viral protein binding partner or partners, involves preparing a reaction mixture containing the host protein and a viral protein under conditions and for a time sufficient to allow the two proteins to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction is conducted in the presence and absence of the test

30   agent. The test agent can be initially included in the reaction mixture, or added at a time subsequent to the addition of a host protein and a viral protein. Controls are incubated without the test agent or with a placebo. Exemplary controls include agents known not to bind to viral or host proteins. The formation of any complexes between the host protein and the viral protein is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test

35   agent, indicates that the agent interferes with the interaction of the host protein and the viral protein, and is therefore possibly an agent that can be used to decrease viral infection.

The assay for agents that interfere with the interaction of host and viral proteins can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring the host protein or the viral protein onto a solid phase and detecting complexes anchored on the solid

76

phase at the end of the reaction. In some examples, the method further involves quantitating the amount of complex formation or inhibition. Exemplary methods that can be used to detect the presence of complexes, when one of the proteins is labeled, include ELISA, spectrophotometry, flow cytometry, and microscopy. In homogeneous assays, the entire reaction is performed in a liquid

5   phase. In either method, the order of addition of reactants can be varied to obtain different information about the agents being tested. For example, test agents that interfere with the interaction between the proteins, such as by competition, can be identified by conducting the reaction in the presence of the test agent, for example by adding the test agent to the reaction mixture prior to or simultaneously with the host protein and viral protein. On the other hand, test agents that disrupt

10   preformed complexes, such as agents with higher binding constants that displace one of the proteins from the complex, can be tested by adding the test agent to the reaction mixture after complexes have been formed. The various formats are described briefly below.

Once identified, test agents found to inhibit or decrease the interaction between a host protein and a viral protein can be formulated in therapeutic products (or even prophylactic products)

15   in pharmaceutically acceptable formulations, and used for specific treatment or prevention of a viral disease, such as HIV, Ebola, or influenza A.

Heterogeneous assay system

In a heterogeneous assay system, one binding partner, either the host protein (such as those

20   listed in Table 1 and target protein sequences associated with SEQ ID NOS: 1-232) or the viral protein (such as an HIV, Ebola, or influenza A virus preparation) is anchored onto a solid surface (such as a microtiter plate), and its binding partner, which is not anchored, is labeled, either directly or indirectly. Exemplary labels include, but are not limited to, enzymes, fluorophores, ligands, and radioactive isotopes. The anchored protein can be immobilized by non-covalent or covalent

25   attachments. Non-covalent attachment can be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody (such as a monoclonal antibody) specific for the protein can be used to anchor the protein to the solid surface. The surfaces can be prepared in advance and stored.

To conduct the assay, the binding partner of the immobilized species is added to the coated

30   surface with or without the test agent. After the reaction is complete, unreacted components are removed (such as by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an

35   indirect label can be used to detect complexes anchored on the surface; for example by using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test agent, the reaction products separated from unreacted components, and complexes detected; for example by using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect

5   anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test agents which inhibit complex or which disrupt preformed complexes can be identified.

Homogenous assays

In an alternate example, a homogeneous assay can be used. In this method, a preformed

10   complex of the host protein and the viral protein is prepared in which one of the proteins is labeled, but the signal generated by the label is quenched due to complex formation (for example, see U.S. Pat. No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test agents that

15   disrupt host protein-viral protein interactions are identified.

Immobilization of Proteins

In a particular example, a host protein involved in viral infection (such as those listed in Table 1 and the target protein sequences associated with SEQ ID NOS: 1-232) can be prepared for

20   immobilization using recombinant DNA techniques. For example, a coding region of a protein listed in Table 1, or any target sequence associated with SEQ ID NOS: 1-232, can be fused to a glutathione-S-transferase (GST) gene using the fusion vector pGEX-5X-1, in such a manner that its binding activity is maintained in the resulting fusion protein. The viral protein (such as an Ebola, HIV, or influenza A protein or viral preparation) can be purified and used to raise a monoclonal antibody,

25   using methods routinely practiced in the art and described above. This antibody can be labeled with the radioactive isotope ^{125}I using methods routinely practiced in the art.

In a heterogeneous assay, for example, the GST-host fusion protein can be anchored to glutathione-agarose beads. The viral protein preparation can then be added in the presence or absence of the test agent in a manner that allows interaction and binding to occur. At the end of the

30   reaction period, unbound material can be washed away, and the labeled monoclonal antibody can be added to the system and allowed to bind to the complexed binding partners. The interaction between the host protein and the viral protein can be detected by measuring the amount of radioactivity that remains associated with the glutathione-agarose beads. A successful inhibition of the interaction by the test compound will result in a decrease in measured radioactivity.

35   Alternatively, the GST-host fusion protein and the viral protein can be mixed together in liquid in the absence of the solid glutathione agarose beads. The test agent can be added either during or after the binding partners are allowed to interact. This mixture can then be added to the glutathione-agarose beads and unbound material is washed away. Again, the extent of inhibition of

the binding partner interaction can be detected by adding the labeled antibody and measuring the radioactivity associated with the beads.

In another example, these same techniques can be employed using peptide fragments that correspond to the binding domains of the host protein and the viral protein, respectively, in place of one or both of the full length proteins. Any number of methods routinely practiced in the art can be used to identify and isolate the protein's binding site. These methods include, but are not limited to, mutagenesis of one of the genes encoding the proteins and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in a host gene can be selected. Sequence analysis of the genes encoding the respective proteins will reveal the mutations that correspond to the region of the protein involved in interactive binding. Alternatively, one protein can be anchored to a solid surface using methods described in above, and allowed to interact with and bind to its labeled binding partner, which has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain may remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the for the cellular or extracellular protein is obtained, short gene segments can be engineered to express peptide fragments of the protein, which can then be tested for binding activity and purified or synthesized.

For example, a host protein can be anchored to a solid material as described above by making a GST-host protein fusion protein and allowing it to bind to glutathione agarose beads. The viral protein can be labeled with a radioactive isotope, such as ^{35}S, and cleaved with a proteolytic enzyme such as trypsin. Cleavage products can then be added to the anchored GST-host protein fusion protein and allowed to bind. After washing away unbound peptides, labeled bound material, representing the cellular or extracellular protein binding domain, can be eluted, purified, and analyzed for amino acid sequence. Peptides so identified can be produced synthetically or fused to appropriate facilitative proteins using recombinant DNA technology.

Example 11

Cell-Based Screening Assay for Agents that Decrease Viral Infection

This example describes methods using intact cells that can be used to screen test agents for their ability to interfere with or even inhibit viral infection of a host cell. For example, a yeast two-hybrid assay or the inverse two-hybrid assay method of Schreiber and coworkers (*Proc. Natl. Acad. Sci., USA* 94:13396, 1977) is used to screen for an agent that disrupts the association between a host protein (such as those listed in Table 1, proteins encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, and any target sequence associated with SEQ ID NOS: 229, 230, and 232) and a viral protein (such as HIV, Ebola, or influenza A virus). Similar to Example 10, therapeutic agents identified by these approaches are tested for their ability to decrease or inhibit infection of a host cell, such as a human cell, by HIV, Ebola, or influenza A.

In one example, the yeast two-hybrid system is used to identify anti-viral agents. One version of this system has been described (Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, 88:9578-82,

1991) and is commercially available from Clontech (Palo Alto, CA). Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one includes the DNA-binding domain of a transcription activator protein fused to one test protein "X" and the other includes the activator protein's activation domain fused to another test protein "Y". Thus, either "X" or "Y" in this system

5   can be a host protein (such as those listed in Table 1 and any target sequences associated with SEQ ID NOS: 1-232), while the other can be a test protein or peptide. The plasmids are transformed into a strain of *Saccharomyces cerevisiae* that contains a reporter gene (such as lacZ) whose regulatory region contains the activator's binding sites. Either hybrid protein alone cannot activate transcription of the reporter gene, the DNA-binding domain hybrid because it does not provide activation function

10   and the activation domain hybrid because it cannot localize to the activator's binding sites. Interaction of the two proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

        The two-hybrid system or related methodology can be used to screen activation domain libraries for proteins that interact with a host protein involved in viral infection. Total genomic or

15   cDNA sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of the host protein involved in viral infection fused to the DNA-binding domain are cotransformed into a yeast reporter strain, and the resulting transformants are screened for those that express the reporter gene. These colonies are purified and the plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the

20   library plasmids.

        For example, and not by way of limitation, a host gene encoding a protein involved in viral infection (such as those listed in Table 1 and target sequences associated with SEQ ID NOS: 1-232) can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. A cDNA library of the cell line from which proteins that interact with

25   the host protein are to be detected can be made using methods routinely practiced in the art. In this particular system, the cDNA fragments can be inserted into a vector such that they are translationally fused to the activation domain of GAL4. This library can be co-transformed along with the host-GAL4 DNA binding domain fusion plasmid into a yeast strain which contains a lacZ gene driven by a promoter which contains GAL4 activation sequences. A cDNA encoded protein, fused to GAL4

30   activation domain, that interacts with the host protein will reconstitute an active GAL4 protein and thereby drive expression of the lacZ gene. Colonies which express lacZ can be detected by their blue color in the presence of X-gal. The cDNA can then be extracted from strains derived from these and used to produce and isolate the host protein-interacting protein using techniques routinely practiced in the art.

35

Example 12

Rapid Screening Assays

        Prior to performing any assays to detect interference with the association of a host protein involved in viral infection and a viral protein such as an HIV, Ebola, or influenza A protein, rapid

screening assays can be used to screen a large number of agents to determine if they bind to the host or viral protein. Rapid screening assays for detecting binding to HIV proteins have been disclosed, for example in U.S. Patent No. 5,230,998, which is incorporated by reference. In that assay, a host protein (such as those listed in Table 1 and target protein sequences associated with SEQ ID NOS: 1-232) or a viral protein, such as an HIV protein, is incubated with a first antibody capable of binding to the host or viral protein, and the agent to be screened. Excess unbound first antibody is washed and removed, and antibody bound to the host or viral protein is detected by adding a second labeled antibody which binds the first antibody. Excess unbound second antibody is then removed, and the amount of the label is quantitated. The effect of the binding effect is then determined in percentages by the formula: (quantity of the label in the absence of the test agent) - (quantity of the label in the presence of the test agent /quantity of the label in the absence of the test agent) x 100.

Agents that are found to have a high binding affinity to the host or viral protein can then be used in other assays more specifically designed to test inhibition of the host protein/viral protein interaction, or inhibition of viral replication.

Example 13

Assays for Measuring Inhibition of Viral Infection

Any of the test agents identified in the foregoing assay systems can be tested for their ability to decrease or inhibit infection by a pathogen or virus such as HIV, Ebola, or influenza A.

Cell-based assays

Exemplary methods are provided in Example 3 above. Briefly, cells (20,000 to 250,000) are infected with the desired pathogen, such as HIV, Ebola, or influenza A, and the incubation continued for 3-7 days. The test agent can be applied to the cells before, during, or after infection with the virus. The amount of virus and agent administered can be determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered, to identify optimal dose ranges. Following transfection, assays are conducted to determine the resistance of the cells to infection by various agents.

For example, the presence of a viral antigen can be determined by using antibody specific for the viral protein then detecting the antibody. In one example, the antibody that specifically binds to the viral protein is labeled, for example with a detectable marker such as a flurophore. In another example, the antibody is detected by using a secondary antibody containg a label. The presence of bound antibody is then detected, for example using microscopy, flow cytometry, and ELISA.

Alternatively or in addition, the ability of the cells to survive viral infection is determined, for example by performing a cell viability assay, such as trypan blue exclusion.

Animal model assays

The ability of an agent, such as those identified using the methods provide above, to prevent or decrease infection by a virus, such as HIV, Ebola, or influenza A, can be assessed in animal

models. Several animal models for viral infection are known in the art. For example, mouse HIV models are disclosed in Sutton *et al.* (*Res. Initiat Treat. Action*, 8:22-4, 2003) and Pincus *et al.* (*AIDS Res. Hum. Retroviruses* 19:901-8, 2003); guinea pig models for Ebola infection are disclosed in Parren *et al.* (*J. Virol.* 76:6408-12, 2002) and Xu *et al.* (*Nat. Med.* 4:37-42, 1998); and cynomolgus

5   monkey (*Macaca fascicularis*) models for influenza infection are disclosed in Kuiken *et al.* (*Vet. Pathol.* 40:304-10, 2003). Such animal models can also be used to test agents for an ability to ameliorate symptoms associated with viral infection. In addition, such animal models can be used to determine the LD50 and the ED50 in animal subjects, and such data can be used to determine the *in vivo* efficacy of potential agents.

10   Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, such as baboons, monkeys, and chimpanzees, can be used to generate an animal model of viral infection if needed.

        The appropriate animal is inoculated with the desired virus, in the presence or absence of the test agents identified in the examples above. The amount of virus and agent administered can be

15   determined by skilled practitioners. In some examples, several different doses of the potential therapeutic agent can be administered to different test subjects, to identify optimal dose ranges. The therapeutic agent can be administered before, during, or after infection with the virus. Subsequent to the treatment, animals are observed for the development of the appropriate viral infection and symptoms associated therewith. A decrease in the development of the appropriate viral infection, or

20   symptoms associated therewith, in the presence of the test agent provides evidence that the test agent is a therapeutic agent that can be used to decrease or even inhibit viral infection in a subject.

        Having illustrated and described the principles of the invention by several examples, it

25   should be apparent that those embodiments can be modified in arrangement and detail without departing from the principles of the invention. Thus, the invention includes all such embodiments and variations thereof, and their equivalents.

We claim:

    1. A method of decreasing infection of a host cell by a virus, comprising interfering with an activity or expression of one or more host proteins or interfering with an activity of one or more host nucleic acids, wherein the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell

5   receptor V-D-J beta 2.1 chain; β-chimerin; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4; v-src sarcoma (Schmidt-

10   Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (LOC57826); LOC161005; osteoblast specific factor 2; Canis familiaris T-cell leukemia translocation-associated protein; aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between LOC253121 and hyaluronan synthase 2; testin 2, testin 3; protein tyrosine phosphatase, non-

15   receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9 (FLJ10402); T-cell receptor beta; similar to murine putative transcription

20   factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; similar to ribosomal protein L24-like (LOC149360); polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2); MGC40489; Rab9; PRO1617; retinoblastoma binding protein 1; region of chromosome 2q12; elongation factor for selenoprotein

25   translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829 ; U3 small nuclear RNA; integrin, beta 1 (ITGB1) ; acrosomal vesicle protein 1

30   (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell

35   surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); Mus musculus 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome-cell adhesion molecule like 1 (DSCAML1); LOC148529; Huntingtin-associated protein interacting protein (HAPIP); LOC158525

and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and hypothetical protein MGC14793; FLJ10439; cytochrome

5   P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase (AXL), and wherein interfering with the activity or expression of the one or more host proteins

10   decreases infection of the host cell by the virus.

       2.   The method of claim 1, wherein the one or more host proteins is encoded by one or more host nucleic acids comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

15

       3.   The method of claim 2, wherein the one or more host nucleic acids comprises any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

       4.   The method of claim 1, wherein the method comprises interfering with an activity or

20   expression of more than one of the host proteins.

       5.   The method of claim 1, wherein the method comprises interfering with an activity or expression of at least three of the host proteins.

25   6.   The method of claim 1 wherein the virus is HIV-1 or HIV-2, and the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β-chimerin; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III; LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-

30   stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins; RAP-2A (LOC57826); LOC161005; Rab9, or osteoblast specific factor 2.

35   7.   The method of claim 6, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

       8.   The method of claim 6, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

84

9. The method of claim 1 wherein the virus is influenza A, and the host protein is a Canis familiaris T-cell leukemia translocation-associated protein, aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between

5   LOC253121 and hyaluronan synthase 2; testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; Rab9, or a myeloid/lymphoma or mixed lineage leukemia, translocated to 10.

10

10. The method of claim 9, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

11. The method of claim 9, wherein the method comprises interfering with expression of

15   one or more of the host nucleic acids.

12. The method of claim 1 wherein the virus is Ebola, and the host protein is a exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C; alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9

20   (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase; MGC40489; Rab9; PRO1617; retinoblastoma binding

25   protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829 ; U3 small

30   nuclear RNA; integrin, beta 1 (ITGB1) ; acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box

35   polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); Mus musculus 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1 (DSCAML1); LOC148529;

Huntingtin-associated protein interacting protein (HAPIP); LOC158525 and similar to RIKEN cDNA
1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory
factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349;
region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and

5   hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide
1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor,
(semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP
citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK);
cyclin M2 (CNNM2); or AXL receptor tyrosine kinase.

10

13. The method of claim 12, wherein the method comprises interfering with an activity or
expression of more than one of the host proteins.

14. The method of claim 12, wherein the method comprises interfering with expression of
15   one or more of the host nucleic acids.

15. The method of claim 6, wherein the one or more host proteins are encoded by one or
more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence
associated with SEQ ID NOS: 1-35.

20

16. The method of claim 6, wherein one or more host proteins is encoded by one or more
nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 1-
35.

25   17. The method of claim 9, wherein the one or more host proteins are encoded by one or
more nucleic acid sequences comprising at least 90% identity to any of SEQ ID NOS: 36-63 or a
coding sequence of any of SEQ ID NOS: 36-63.

18. The method of claim 9, wherein the one or more host proteins are encoded by one or
30   more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID
NOS: 36-63.

19. The method of claim 12, wherein the one or more host proteins are encoded by one or
more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence
35   associated with SEQ ID NOS: 64-227, 229, and 231.

20. The method of claim 12, wherein one or more host proteins are encoded by one or more
nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS:
64-227, 229, and 231.

21. The method of claim 1, wherein interfering with the activity of the one or more host proteins comprises decreasing an interaction of a viral protein and the one or more host proteins by disrupting or decreasing expression of the one or more host proteins.

5

22. The method of claim 21, wherein the viral protein comprises a virus and decreasing the interaction of the viral protein and the one or more host proteins decreases or inhibits infection of a host cell by the virus.

10   23. The method of claim 21, wherein disrupting or decreasing expression of the host protein comprises disrupting or decreasing transcription of an mRNA encoding the host protein.

24. The method of claim 23, wherein disrupting or decreasing transcription of the mRNA comprises inserting a transposon or insertional vector into a coding region of the nucleic acid

15   encoding the host protein.

25. The method of claim 23, wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, RNAi, ribozyme, or siRNA that recognizes the mRNA.

20

26. The method of claim 1 wherein interfering with the activity of the host protein comprises decreasing an interaction of a viral protein and the host protein by contacting the cell with an agent that decreases or inhibits the activity or expression of the host protein or that disrupts expression of the host protein.

25

27. The method of claim 26, wherein the host cell is present in a host subject and wherein contacting the cell with the agent comprises administering the agent to the subject.

28. The method of claim 1, wherein the host cell is a mammalian host cell.

30

29. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising, decreasing an interaction between a viral nucleic acid and a host nucleic acid by decreasing the integration of the viral nucleic acid into the host nucleic acid, wherein the host nucleic acid comprises at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

35

30. The method of claim 29, wherein the viral nucleic acid comprises a viral genome and the host nucleic acid comprises a host genome.

31. A method of treating an HIV, Ebola, or influenza A viral infection in a host subject, comprising administering to a subject having a viral infection an effective amount of an agent that interferes with the interaction of a virus and host protein, wherein the host protein is encoded by a nucleic acid comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

32. The method of claim 31, wherein the agent disrupts expression of the nucleic acid encoding the host protein.

33. The method of claim 32, wherein the agent is an antisense, ribozyme, or siRNA molecule that recognizes the nucleic acid sequence comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

34. The method of claim 31, wherein the effective amount induces a prophylactic effect in the host, which inhibits infection of the host by a virus.

35. The method of claim 31, wherein the host was previously infected by a virus and the effective amount induces a therapeutic effect in the host.

36. A method of determining resistance or susceptibility to viral infection in a subject, comprising comparing a first nucleic acid sequence of a subject to a second nucleic acid sequence comprising any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, wherein a higher similarity between the first and second nucleic acid sequence indicates the subject is more susceptible to viral infection, and wherein a lesser similarity between the first and second nucleic acid sequence indicates the subject is more resistant to viral infection.

37. The method of claim 36, wherein the first nucleic acid sequence is obtained from a biological sample of the subject.

38. The method of claim 37, wherein the first nucleic acid sequence comprises a plurality of nucleic acid sequences, wherein each nucleic acid sequence is obtained from a different subject.

39. The method according to claim 36, further comprising determining a polymorphic variation within a population.

40. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising:
contacting the host cell with an anti-protein binding agent that selectively or specifically binds to a host protein encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231 or a protein sequence shown in any of SEQ ID NOS: 228, 230, or 232, wherein the anti-protein

88

binding agent inhibits an interaction between the host protein and the HIV, Ebola, or influenza A virus.

41. The method of claim 40, wherein the host cell is present in a subject, and contacting the host cell with the anti-protein binding agent comprises administering the anti-protein binding agent to the subject.

42. The method of claim 40, wherein the anti-protein binding agent is an antibody or chemical compound.

43. A method of identifying a compound that decreases binding of a viral protein to a host protein and decreases viral infection, comprising:

contacting the host protein with the viral protein and a test compound, wherein the host protein is a protein in Table 1, and the viral protein is an HIV, Ebola, or influenza A protein; and

determining whether binding of the viral protein to the host protein is decreased in the presence of the test compound, the decrease in binding being an indication that the test compound decreases the binding of viral protein to the target protein, and decreases viral infection.

44. The method of claim 43, wherein the viral protein comprises a virus.

45. The method of claim 43, wherein the viral protein is a viral envelope protein.

46. The method of claim 43, wherein the viral protein is an HIV protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 1-35.

47. The method of 43, wherein the viral protein is an influenza A protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 36-63.

48. The method of claim 43, wherein the viral protein is an Ebola protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 64-227, 229, and 231.

49. The method of claim 43, wherein the method comprises expressing the host protein in a cell, and contacting the host protein with the viral protein and a test compound comprises exposing the cell to the viral protein and the test compound.

50. The method of claim 43, wherein the host protein or the viral protein comprises a label, and determining whether binding is decreased comprises detecting an amount of label present.

51. A method of decreasing infection of a host cell by a pathogen, comprising interfering with an activity or expression of a Rab9 in the host cell, wherein interfering with Rab9 activity or expression decreases infection of the host cell by the pathogen.

5   52. The method of claim 51, wherein the pathogen hijacks a lipid raft.

53. The method of claim 51, wherein the pathogen is a *Campylobacter jujuni*, *Vibrio cholerae*, SV40, *Legionella pneumophila*, *Aeromonas hydrophilia*, Echovirus 1, Echovirus 11, *Brucella* spp, *Clostridium* spp., Avian sarcoma and leukosis virus, FimH, Dr *Escherichia coli*, 10   *Streptcoccus pyogenes*, Semiliki forest virus, *Salmonella typhimurium*, *Bacillus anthracis*, Ecotropic mouse leukaemia virus, *Shigella flexneri*, *Bacillus thuringiensis*, HTLV-1, *Chlamydia* spp., *Helicobacter pylori*, HIV-1, *Mycobacterium* spp., *Lysteria monocytogenes*, *Ebola*, *Marburg*, Measles, Herpes Simplex virus, influenza virus, or Epstein-Barr virus.

15   54. The method of claim 51, wherein the Rab9 host protein is encoded by a host nucleic acid comprising at least 90% identity to a target sequence associated with any of SEQ ID NOS: 118-119.

55. The method of claim 54, wherein the host nucleic acid comprises a target sequence 20   associated with any of SEQ ID NOS: 118-119.

56. The method of claim 51, wherein interfering with expression of Rab9 comprises disrupting or decreasing transcription of an mRNA encoding the Rab9 protein.

25   57. The method of claim 56 wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA.

58. The method of claim 57, wherein the siRNA sequence comprises any of SEQ ID NOS: 30   232-235.

59. The method of claim 57, wherein the host cell is present in a subject, and contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA comprises administering the antisense RNA, ribozyme, or siRNA to the subject.

35

60. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the cell has a decreased susceptibility to HIV infection.

90

61. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the cell has a decreased susceptibility to influenza infection.

62. A cell comprising a functional deletion of one or more target sequences associated with 5 any of SEQ ID NOS: 64-232, wherein the cell has a decreased susceptibility to Ebola infection.

63. A cell comprising a functional deletion of a Rab9 gene, wherein the cell has a decreased susceptibility to infection by a pathogen that uses lipid rafts.

10   64. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the mammal has decreased suseptibility to infection by HIV.

65. A non-human transgenic mammal comprising a functional deletion of one or more 15 target sequences associated with any of SEQ ID NOS: 36-63, wherein the mammal has decreased suseptibility to infection by influenza.

66. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the mammal has decreased 20 suseptibility to infection by Ebola.

67. A non-human transgenic mammal comprising a functional deletion of a Rab9 gene, wherein the mammal has decreased suseptivlity to infection by a pathogen that uses a lipid raft.

25   68. The method of claim 1, wherein interfering with an activity of the host nucleic acid comprising administering one or more of SEQ ID NOS: 246- 845 to the host cell.
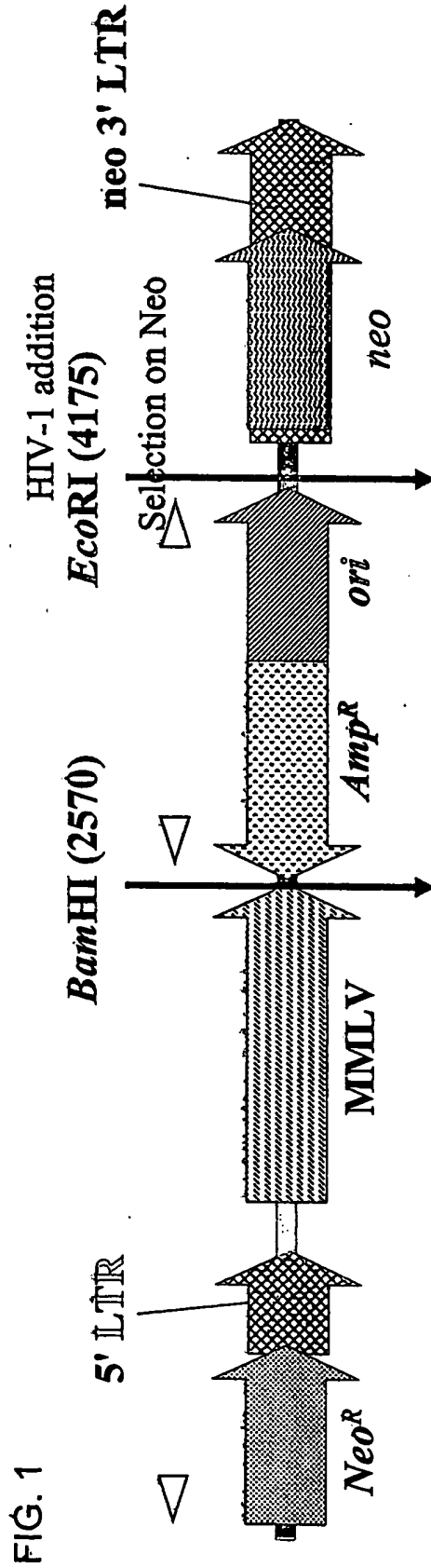
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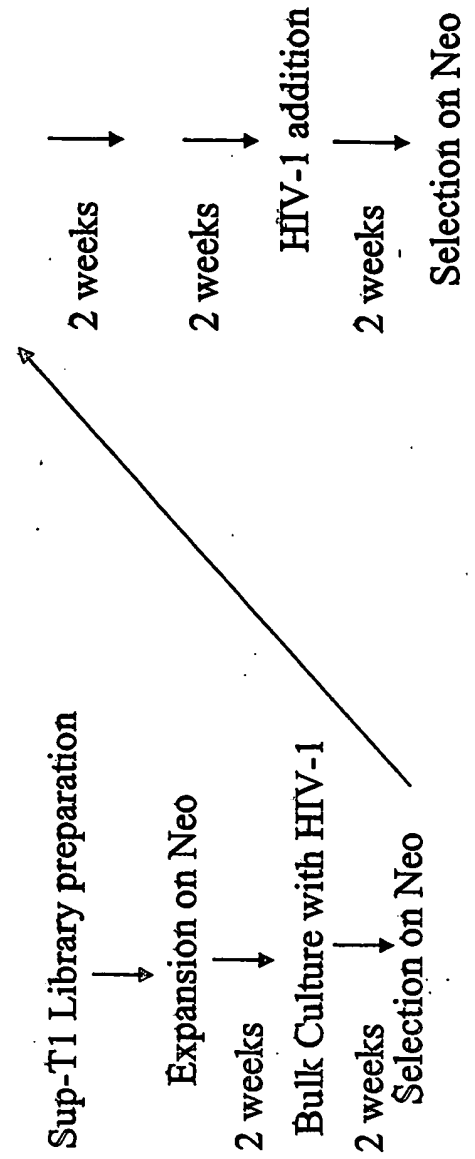
FIG.4

FIG. 2

FIG. 3

FIG. 5

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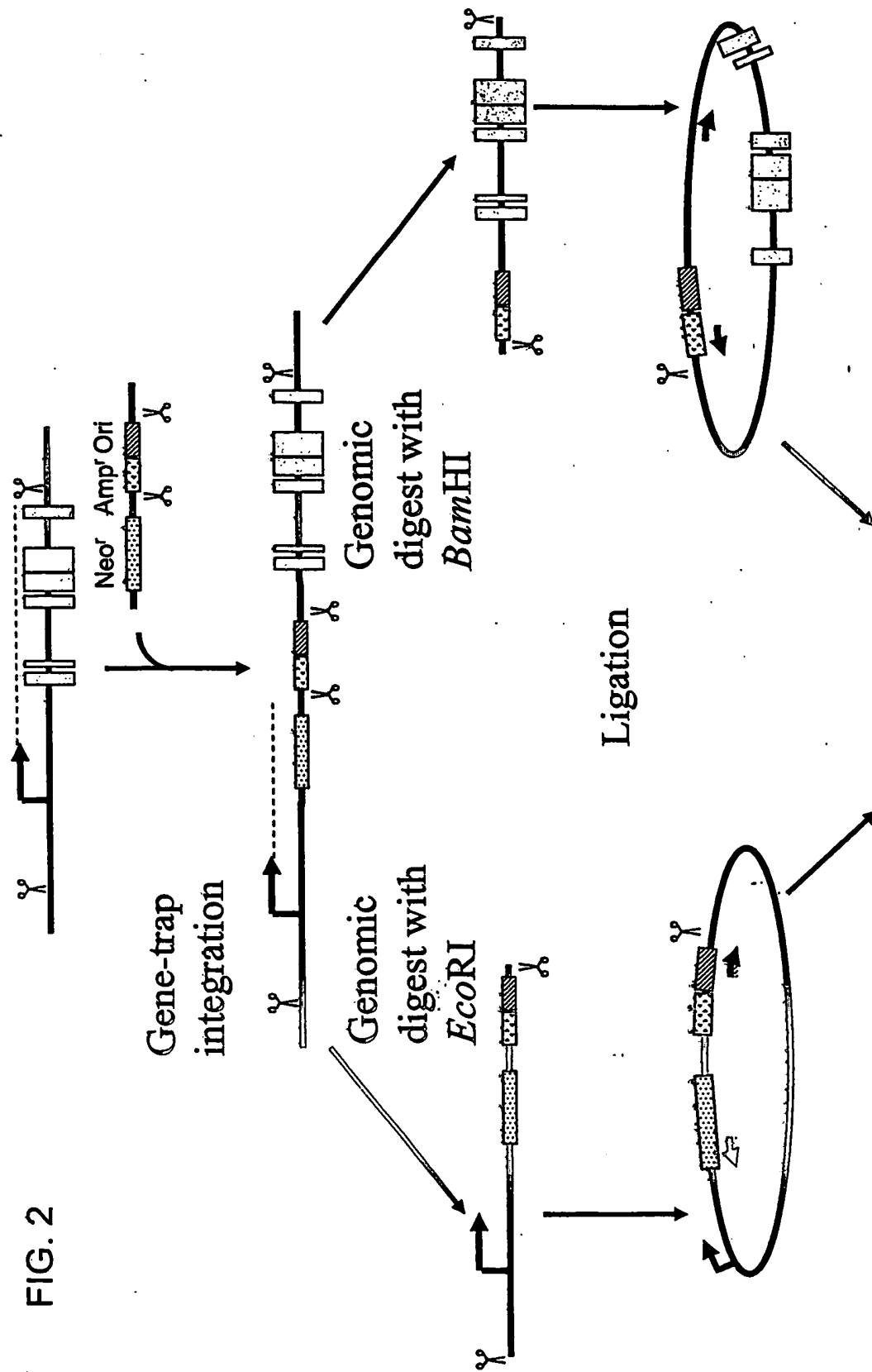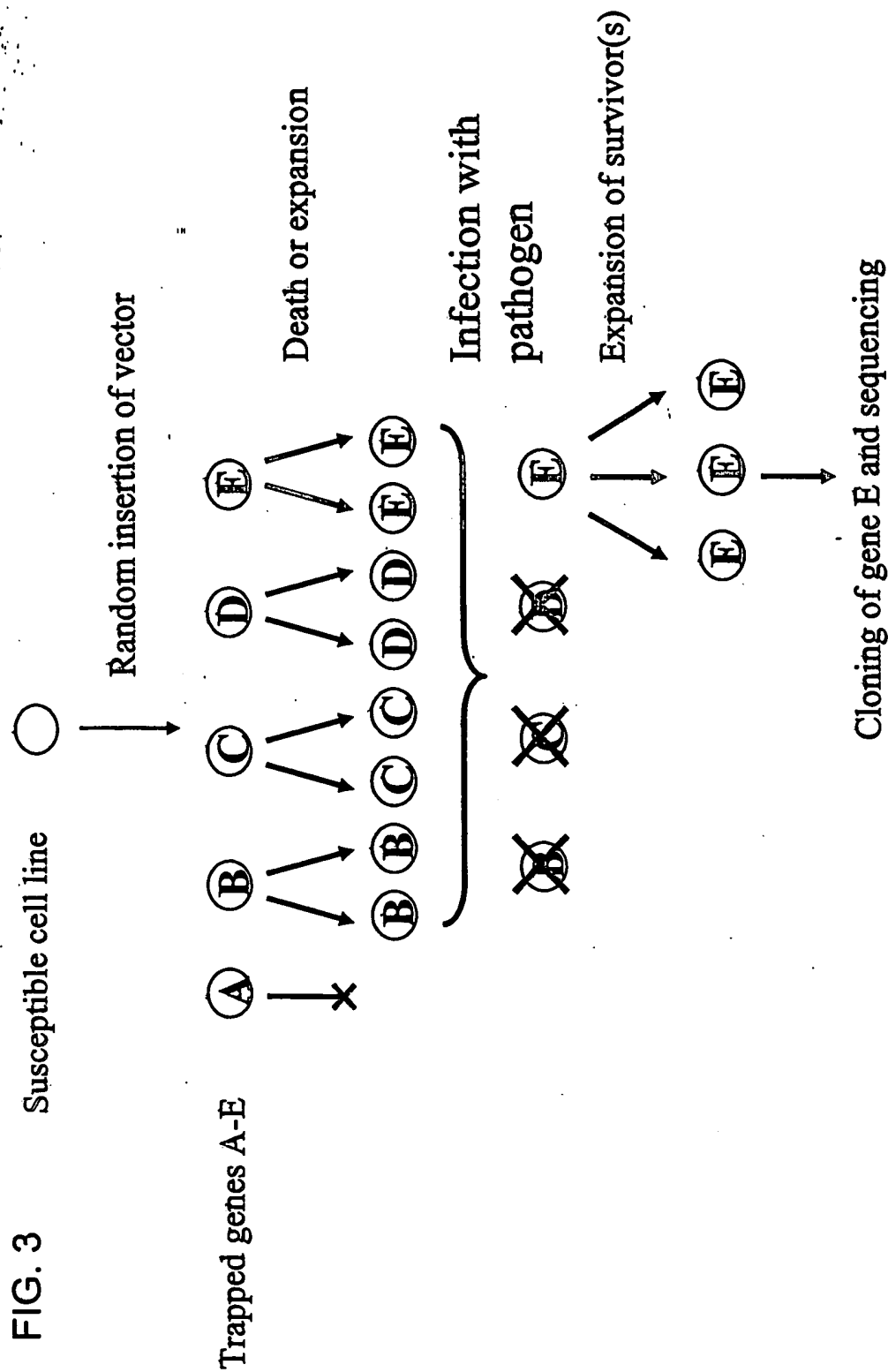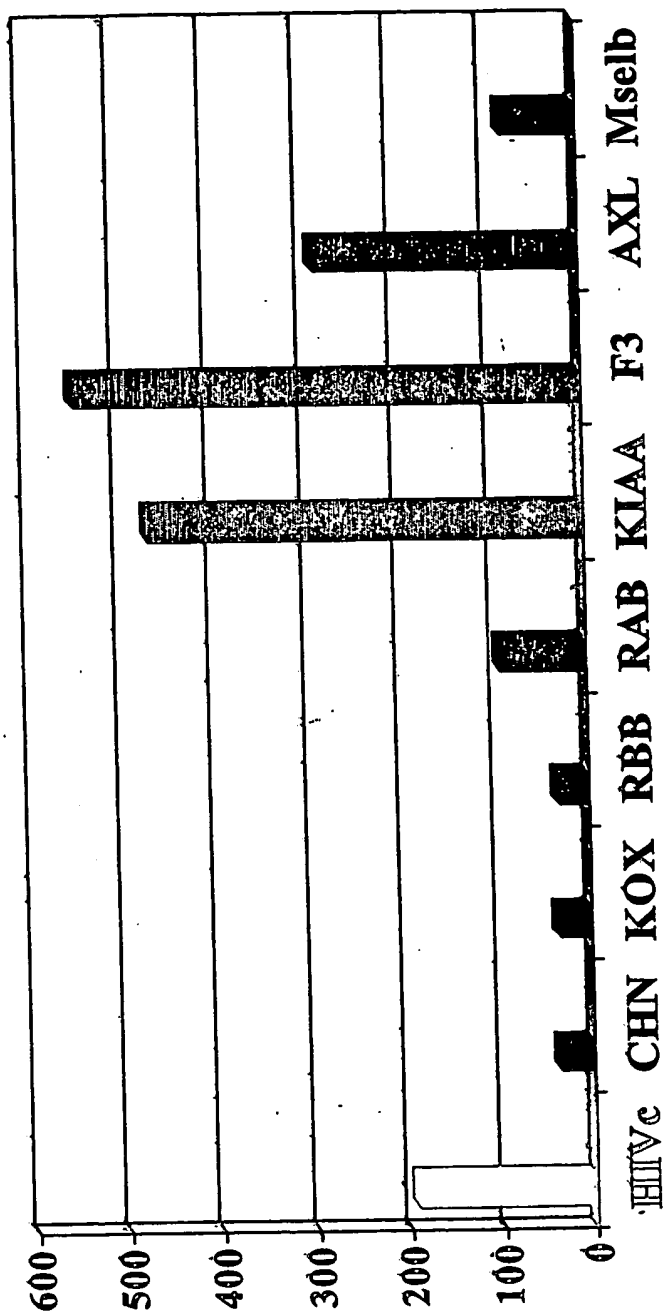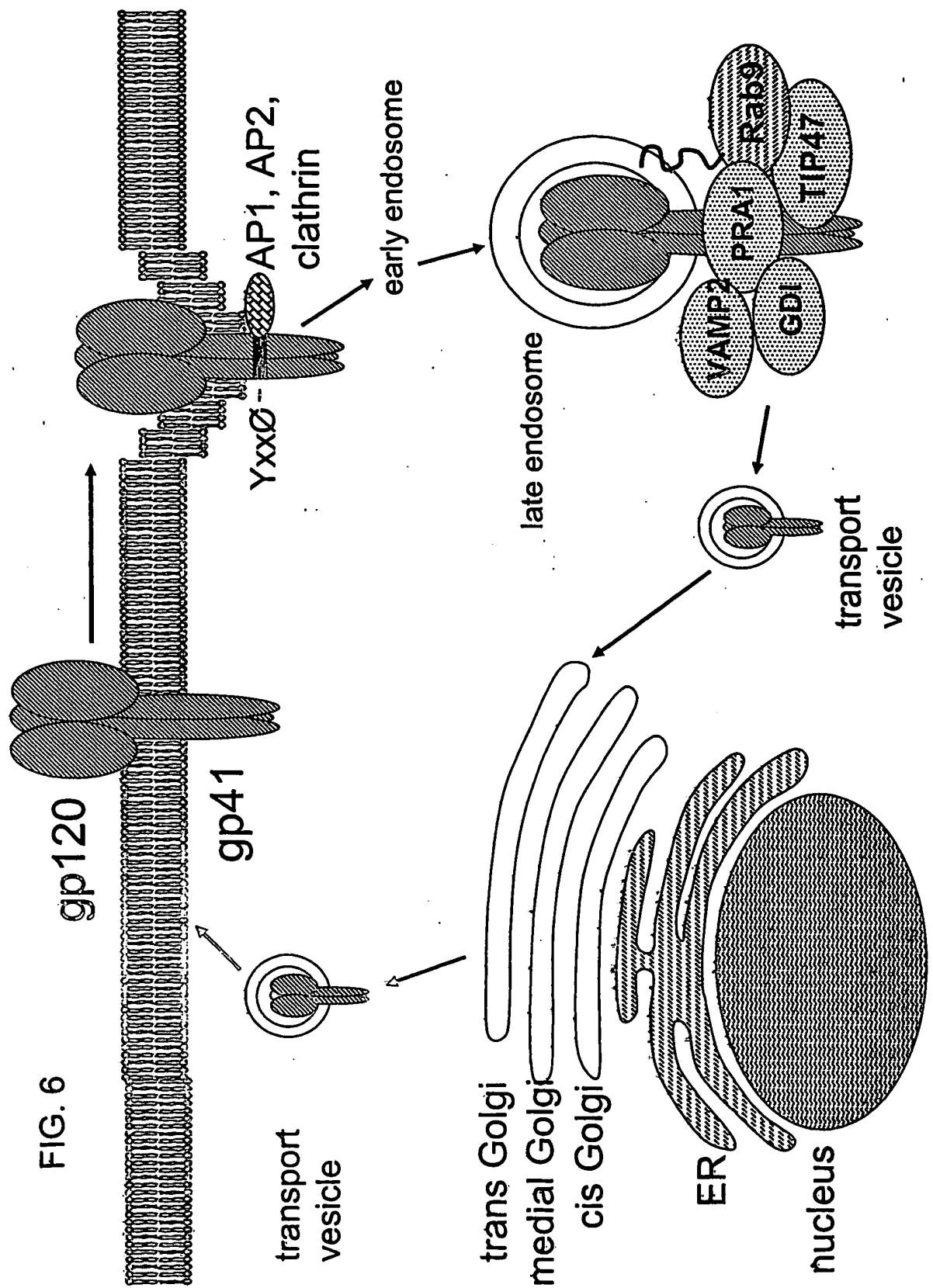
STATEMENT ACCOMPANYING SEQUENCE LISTING

The sequence listing does not include matter that goes beyond the disclosure in the international application.

The printout of the attached Sequence Listing is identical to the computer readable sequence listing on the enclosed computer disk.

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ctactccatg ctaagttcag cgagaacttg gggtaccta gacattcttc cagagatgct      180
tttcttgtaa ctcttttcaa taagtaagca tgctttgctc tgcactgggt gtcacctgtg     240
ttggatgctg ttgtccctgc cttgccctat attctgtcca catggtttct tcataggatg     300
atgcttaggt cagccctgag gtttgaacca gtcaacaagt ccaggttggt gtggagtccc     360
tttagtacct ccctttgcag gaataatgct gcacccagaa actccctcag agcctctcca     420
ctggaggggc cttgtgacca ttcctggttt actcctcttg ttccagcatc ccatgtggcc     480
aatgggcccc tttcattttc aatggtatct caattcttac agtaagttat attattgccc     540
tacatcgaac tcatcttttc tcagtgttac ctgaggaaga atggagagga tgcccagaat     600
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tggcccagaa gaatccactt cgattctaga gaaaaaggca ggtagaggca gaagagattc   660

acttcccagt gcatgcgtgc tgaatgttgg gggtgttgtt tgagagagac aaggaaatgg   720

ctgtaaaact tgggaagagg aacctgccct gggtcaagta gggtgttggg aggaccagat   780

ggagcttgaa gctctctcca tctttgtcaa gtcccctgga ctgagagggn aaaatnacat   840

ggcctttatc ctccagagga aantnattc   869

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<211>   850
<212>   DNA
<213>   Homo sapiens

<220>
<221>   misc_feature
<222>   (1)..(850)
<223>   n is a, g, c, or t

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gagttcttct gagcgggact ctggggttcg aaatgagcta gcccttaagt aacgccattt   120

tgcaaggcat ggaaaaatac ataactgaga atagaaaagt tcagatcgag gtcaggaaca   180

gatggaacag ggtcgaccgg tcgaccggtc gaccctagag aaccatcaga tgtttccagg   240

gtgccccaag gacctgaaat gaccctgtgc cttatttgaa ctaaccaatc agttcgcttc   300

tcgcttctgt tcgcgcgctt ctgctccccg agctcaataa aagagcccac aacccctcac   360

tcggggcgcc agtcctccga ttgactgagt cgcccgggta ccgtgtatc caataaaccc   420

tcttgcagtt gcatccgact tgtggtctcg ctgttccttg ggagggtctc ctctgagtga   480

ttgactaccc gtcagcgggg gtctttcact ctctgtgtac tggtaccaac agagcctgga   540

ccagggcctc cagttcctca ttcagtatta taatggagaa gagagagcaa aaggaaacat   600

tcttgaacga ttctccgcac aacagttccc tgacttgcac tctgaactaa acctgagctc   660

tctggagctg ggggactcag ctttgtattt ctgtgccagc agcgtaggtg gtagcttgaa   720

acagttcttc gggccaggga cacggctcac cgtgctaggt aagaaggggg ctccaggtgg   780

gagagagggt gagcagccca ncctgcacga ccccanaacc ctgttcttag gggagnggac   840

actgggncat   850

<210>   7
<211>   847
<212>   DNA
<213>   Homo sapiens

                                                 5

<220>
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<222> (1)..(847)
<223> n is a, g, c, or t

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gagcatctca gcgtcactcg ctgtccagtt gctgtgatca ggtgctttgg ggtttgtgtg   120

actccagaat ccactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag   180

aaagcctcct gctgaagcca tcgttggccc acatgcattt cagggacaag aaatgaagat   240

cggagacttt caagttgtgc ccaggactca cctgctccca ggagacaaaa ggccacacag   300

cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctggtgtc tctgtagtaa   360

gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc   420

acactgacat actttcccct gcaggccact ccagcccact gtactctttg gcaggcctca   480

ggttctgcta ctccatgtac tattcctgtc ttgcacaggc cagaagctaa aggtgaggag   540

gactgaacac agtaccaaca tacccacatc acaccttact ttcctctgcc cgccctgtcc   600

ctgccctgac actgattccc cagcccttgc caccccagcc ccttcaccct ccactgcccg   660

tgcagcagca gagacactcc ctccttgatg caaactgagg cctctggcac cccaactctt   720

tcagggcaat gatagtctgt gcttaactct acatggccag gccccactca gggaattctc   780

acctagaatt tcatatncag ccaaactaag cttcataagt gaaggggaaa taaaatgctt   840

tacagac   847

<210>   8
<211>   755
<212>   DNA
<213>   Homo sapiens

<220>
<221>   misc_feature
<222>   (1)..(755)
<223>   n is a, g, c, or t

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taagtgcaag tttatttta tttttttttt ttttttgaga cagagtctcg ctctgtcacc   120

caggctagag tgcagtggca tgatcttggc tcactgcaac ctccacctcc caggttcaag   180

tgattctctt gcctcagcct cccaagtagc tagtattaca gacgcctgcc accacgcccg   240

gttaattttt gtacttttag tagagacagg tttcaccata ttggccaggc tggtctcaaa   300

ctcctgacct caggtgatcc tcctgcctca gcctcccaaa gtgctgggat tacaggcatg   360

agctaccacg tctggcctaa gtgcatgtta cctatactaa caaaaccaca cttctgcctc   420

gaatgagaac agtctcctga acatcttgcc tctttgcctg actcaaagcc tcaggtctaa   480

gcctccccat aatttctagt ctcagcagaa agatcaatga caggagactc tccaggtgat   540

gaaattaacc aattaagtaa cctgggttgg catcctcccg tttgttcacc agctcacctn   600

ctgccacagg tatatccttt ctctcancca tatatgcaca aaccccctnc ccacggnaca   660

catannaana atttggaaga ctanaaaatc aggcanggtn tancncacct tgngggctgg   720

agtatggnan cctgggccgg nacatncata cattg   755

<210> 9
<211> 839
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(839)
<223> n is a, g, c, or t

<400> 9
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accttcacta caaggatatt acaacaggac attttttaaa acctcaaaca tcaccaaaat   120

ttctaagtgc aagtttattt ttattttttt tttttttttt gagacagagt ctcgctctgt   180

cacccaggct agagtgcagt ggcatgatct tggctcactg caacctccac ctcccaggtt   240

caagtgattc tcttgcctca gcctcccaag tagctagtat tacagacgcc tgccaccacg   300

cccggttaat ttttgtactt ttagtagaga caggtttcac catattggcc aggctggtct   360

caaactcctg acctcaggtg atcctcctgc ctcagcctcc caaagtgctg ggattacagg   420

catgagctac cacgtctggc ctaagtgcat gttacctata ctaacaaaac cacacttctg   480

cctcgaatga gaacagtctc ctgaacatct tgcctctttg cctgactcaa agcctcaggt   540

ctaagcctcc ccataatttc tagtctcagc agaaagatca atgacaggag actctccagg   600

tgatgaaatt aaccaattaa gtaacctggg ttggcatcct cccgtttgtt caccagctca   660

cctcctgcca caggtatatc ctttctctca gccatatatg cacaaacccc ctccccacgg   720

cacacataga aanaatttgg aagactagaa aatcaggcna gggnttanca caccttngag   780

ggctggagta tggnanccng ggnccgggan atncatncnn tngaaaactt gactatggg   839

<210> 10
<211> 829
<212> DNA
<213> Homo sapiens

7

<220>
<221> misc_feature
<222> (1)..(829)
<223> n is a, g, c, or t

<400> 10
tcgccttcaa tcgtcttatt nacgagttct tctgagcggg actctggggt tcgaaatgag   60

ctagcccttta agtaacgcca ttttgcaagg catggaaaaa tacataactg agaatagaaa   120

agttcagatc gaggtcagga acagatggaa cagggtcgac cggtcgaccg gtcgacccta   180

gagaaccatc agatgtttcc agggtgcccc aaggacctga aatgaccctg tgccttattt   240

gaactaacca atcagttcgc ttctcgcttc tgttcgcgcg cttctgctcc ccgagctcaa   300

taaaagagcc cacaacccct cactcggggc gccagtcctc cgattgactg agtcgcccgg   360

gtacccgtgt atccaataaa ccctcttgca gttgcatccg acttgtggtc tcgctgttcc   420

ttgggagggt ctcctctgag tgattgacta cccgtcagcg ggggtctttc agtagccctt   480

cctttgtagc aaagacagac agatggtgat ccaagagata cgcaagaaga ggaccgtgtg   540

tgtcatggtt gagctctaaa aaagagaaat cacttggatg gaantgaagg agaggaaaag   600

gctgatgtgg atggcctgga agangttcga ttggttacct tggcaccgag cttccttcct   660

catcctcatn cctccctagt ccttgttctt aaaaanantt ttctttctaa ngtcccttcc   720

ccctccncaa gggggcacaa ggatntttaa aaaacncctt tccgggcnta attttaacct   780

angatccatc ccagnccgt nccnnttttc nnagattcat ttaaacnng   829

<210> 11
<211> 710
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(710)
<223> n is a, g, c, or t

<400> 11
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tgacgagttc ttctgagcgg gactctgggg ttcgaaatga gctagccctt aagtaacgcc   120

attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg   180

aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaaccat cagatgtttc   240

cagggtgccc caaggacctg aaatgaccct gtgccttatt tgaactaacc aatcagttcg   300

cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc   360

tcactcgggg cgccagtcct ccgattgact gagtcgcccg ggtacccgtg tatccaataa   420

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accctcttgc agttgcatcc gacttgtggt ctcgctgttc cttgggaggg tctcctctga      480

gtgattgact acccgtcagc gggggtcttt cagtagccct tcctttgtag caaagacaga      540

cagatggtga tccaagagat acgcaagaag aggaccgtgt gtgtaatggt tgagctctaa      600

aaagagaaat cacttggatg gaaatgaagg agaggaaagg ctgatgtgga tggctgggaa      660

gaggttcgat ggttaccttg gcanccganc ttcnttnctn atncccatcc                 710
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<210>   12
<211>   752
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(752)
<223>   n is a, g, c, or t

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aggcaactct ctcttcccac ctgcccccca aactcccttc cacctccctc cacatgtatc      120

ctcccacttc cttccactca tgtaatgaga ggtgctgatg agtcacagga gaggtagccc      180

tagataacca acagactgca aaacggacag tccctggatg tctgagccag tgtttgtgca      240

ctgcattgac tggctcctcg tagtttttc ctgtagttgc taaagcctgt aaggtctgtg      300

tgatgaatat tttctaacac atcttagaag aacataatgc aagacagaat gaaaaactag      360

agaggcagaa accccccaaag taagtagtgg gaaattacca ggtatataat aggtcaagcc     420

tgctctgcag gagctcaagg gattgtagca ttcttatccc aaaccactga atcctgggca      480

aaaataagaa gtcgcctaat tttagtatta ccagcttccc aaccccgggc attcttcatc      540

ttactcaagc tgtccagagg ccccagggtg actccctata agtcccatgg gtggctgaga      600

tctatttaga ggcacaaggg tatctnctta taagtccaat ggggnggctg agatctatga      660

gaagcatctt gggggagagt gccntttggc caccagcatg tggnccctna attttncatg      720

nnncaactgg nccngggaag gaaaantttt ga                                    752
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<210>   13
<211>   749
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(749)
<223>   n is a, g, c, or t
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9

<400> 13

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ttgacgagtt cttctgagcg ggactctggg gttcgaaatg agctagccct taagtaacgc   120

cattttgcaa ggcatggaaa aatacataac tgagaataga aaagttcaga tcgaggtcag   180

gaacagatgg aacagggtcg accggtcgac cggtcgaccc tagagaacca tcagatgttt   240

ccagggtgcc ccaaggacct gaaatgaccc tgtgccttat ttgaactaac caatcagttc   300

gcttctcgct tctgttcgcg cgcttctgct ccccgagctc aataaaagag cccacaaccc   360

ctcactcggg gcgccagtcc tccgattgac tgagtcgccc gggtacccgt gtatccaata   420

aaccctcttg cagttgcatc cgacttgtgg tctcgctgtt ccttgggagg gtctcctctg   480

agtgattgac tacccgtcag cgggggtctt tcagtagccc ttcctttgta gcaaagacag   540

acagatggtg atccaagaga tacgcaagaa gaggaccgtg tgtgtaatgg ttgagcttta   600

aaaaangaga aatcacttgg atggaaatga agganaggaa aaggcntgat ntngatngcn   660

gggaaanagg ttccatnggt nncttggnn anccgannct tnctttcctn atccccntnc   720

cntccctann nccntnnttn ttaaaaaag   749

<210>   14
<211>   794
<212>   DNA
<213>   Homo sapiens

<220>
<221>   misc_feature
<222>   (1)..(794)
<223>   n is a, g, c, or t

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ttgacgagtt cttctgagcg ggactctggg gttcgaaatg agctagccct taagtaacgc   120

cattttgcaa ggcatggaaa aatacataac tgagaataga aaagttcaga tcgaggtcag   180

gaacagatgg aacagggtcg accggtcgac cggtcgaccc tagagaacca tcagatgttt   240

ccagggtgcc ccaaggacct gaaatgaccc tgtgccttat ttgaactaac caatcagttc   300

gcttctcgct tctgttcgcg cgcttctgct ccccgagctc aataaaagag cccacaaccc   360

ctcactcggg gcgccagtcc tccgattgac tgagtcgccc gggtacccgt gtatccaata   420

aaccctcttg cagttgcatc cgacttgtgg tctcgctgtt ccttgggagg gtctcctctg   480

agtgattgac tacccgtcag cgggggtctt tcagtagccc ttcctttgta gcaaagacag   540

acagatggtg atccaagaga tacgcaagaa gaggaccgtg tgtgtaatgg ttgagctcta   600

aaaagagaa atcacttgga tggaaatgaa ggagaggaaa aggctgatgt ggatggctgg   660

gaagaggttc gatggttacc ttggcaaccg agcttccttn ctcatnccca tccctnccta   720

gtccttgttc tttaaaaaga ttttntttnt aatgtccctt nccctccaca aggggcaca   780

agatgttttn aaac   794

<210> 15
<211> 784
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(784)
<223> n is a, g, c, or t

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agttctcagg gngaacaaaa aattgtatgt gtgcagaacc tgtgatttgc ctgcacatag   120

tcaagttctc aatgtatgga tgtcccggcc caggctacca tactccagcc ctcaaggtgt   180

gctatacctt gcctgatttt ctagtcttcc aaattcttct atgtgtgccg tggggagggg   240

gtttgtgcat atatggctga gagaaaggat atacctgtgg caggaggtga gctggtgaac   300

aaacgggagg atgccaaccc aggttactta attggttaat ttcatcacct ggagagtctc   360

ctgtcattga tctttctgct gagactagaa attatgggga ggcttagacc tgaggctttg   420

agtcaggcaa agaggcaaga tgttcaggag actgttctca ttcgaggcag aagtgtggtt   480

ttgttagtat aggtaacatg cacttaggcc agacgtggta gctcatgcct gtaatcccag   540

cactttggga ggctgaggca ggaggatcac ctgaggtcag gagttttgag accagcctgg   600

ccaatatggg ggaaaacctg tctctactaa aaagtacaaa aattaacccg gncgtnggng   660

gcaggnnntc tgtaatacta nnctacttgg gngngtgnag gcaanaaaat cantttgaac   720

ctnggnaggg gggngnttgc aatnnnccna aaaanatgcc cnntggncct ttaaccntgg   780

gngn   784

<210> 16
<211> 757
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(757)
<223> n is a, g, c, or t

<400> 16

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acatttttta aaacctcaaa catcaccaaa atttctaagt gcaagtttat ttttattttt    120

ttttttttt ttttgagaca gagtctcgct ctgtcaccca ggctagagtg cagtggcatg     180

atcttggctc actgcaacct ccacctccca ggttcaagtg attctcttgc ctcagcctcc    240

caagtagcta gtattacaga cgcctgccac cacgcccggt taattttgt actttagta     300

gagacaggtt tcaccatatt ggccaggctg gtctcaaact cctgacctca ggtgatcctc    360

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gcatgttacc tatactaaca aaaccacact tctgcctcga atgagaacag tctcctgaac    480

atcttgcctc tttgcctgac tcaaagcctc aggtctaagc ctccccataa tttctagtct    540

tgggttggca tcctcccgtt tgttcaccag ctcacctnct gncacaggta tatncttttt    660

tctnagccat atatgcccaa anccccctnc ccacggnaca catngaagaa nttnggaaga    720

ctngaaaatc aggccagggt tnngcccacc ttgnggg                             757
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<210>   17
<211>   783
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(783)
<223>   n is a, g, c, or t

<400>   17
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tacaacagga catttttttt aacctnaaac attaccacaa atttctaagt gcaagtttat    120

ttttattttt ttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtgca    180

gtggcatgat cttggctcac tgcaacctcc acctcccagg ttcaagtgat tctcttgcct    240

cagcctccca agtagctagt attacagacg cctgccacca cgcccggtta attttgtac     300

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tgatcctcct gcctcagcct cccaaagtgc tgggattaca ggcatgagct accacgtctg    420

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aagtaacctg ggttggcatc ctcccgtttg ttcaccagct cacctcctgc cacaggtata    660

tcctttctct cagccatata tgcacaaacc ccctncccac ggcacacata gaagaatttg    720
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gaagactaga aaatcaggca nggtatagca caccttggag ggctggagta tggtagcctg   780

ggc   783

<210> 18
<211> 770
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(770)
<223> n is a, g, c, or t

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acattttta aaacctcaaa catcaccaaa atttctaagt gcaagtttat ttttattttt   120

tttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtgca gtggcatgat   180

cttggctcac tgcaacctcc acctcccagg ttcaagtgat tctcttgcct cagcctccca   240

agtagctagt attacagacg cctgccacca cgcccggtta atttttgtac ttttagtaga   300

gacaggtttc accatattgg ccaggctggt ctcaaactcc tgacctcagg tgatcctcct   360
gcctcagcct cccaaagtgc tgggattaca ggcatgagct accacgtctg cctaagtgc   420

atgttaccta tactaacaaa accacacttc tgcctcgaat gagaacagtc tcctgaacat   480

cttgcctctt tgcctgactc aaagcctcag gtctaagcct ccccataatt tctagtctca   540

gcagaaagat caatgacagg agactctcca ggtgatgaaa ttaaccaatt aagtaacctg   600

ggttggcatc ctcccgtttg ttcaccagct cacctnctgc cacaggtata tccttttct   660

tagccatata tgcacaaacc ccctcccac ggnacacata gaaaaatttn ggaagactag   720

aaaatcaggc agggtntagc acaccttngn gggctnggag tntnggtanc   770

<210> 19
<211> 774
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(774)
<223> n is a, g, c, or t

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acattttta aaacctcaaa catcaccaaa atttctaagt gcaagtttat ttttattttt   120

tttttttttt ttgagacaga gtctcgctct gtcacccagg ctagagtgca gtggcatgat   180

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cttggctcac tgcaacctcc acctcccagg ttcaagtgat tctcttgcct cagcctccca    240

agtagctagt attacagacg cctgccacca cgcccggtta attttgtac ttttagtaga     300

gacaggtttc accatattgg ccaggctggt ctcaaactcc tgacctcagg tgatcctcct    360

gcctcagcct cccaaagtgc tgggattaca ggcatgagct accacgtctg gcctaagtgc    420

atgttaccta tactaacaaa accacacttc tgcctcgaat gagaacagtc tcctgaacat    480

cttgcctctt tgcctgactc aaagcctcag gtctaagcct ncccataatt tctagtctca    540

gcagaaagat caatgacagg agactctnca ggtgatgaaa ttaaccaatt aagtaacctg    600

ggttggcatc ctcccgtttg ntcaccagnc tnacctnctg ncacaggnat atnctttnt     660

ttnagccata tntgcacaaa cccccctnccc acggnacaca tagaaaaant tnggnagact   720

ngaaaattca ggncagggnt tagcncnccc ttgggggnnt ggnntntngg aacc          774
```

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<210>  20
<211>  914
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (1)..(914)
<223>  n is a, g, c, or t

<400>  20
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tggggntncc ggtatcgccg cttccgattc gcagcgcatc gccttctatc gccttcttga    60

cgagttcttc tgagcgggac tctggggttc gaaatgagct agcccttaag taacgccatt    120

ttgcaaggca tggaaaaata cataactgag aatagaaaag ttcagatcga ggtcaggaac    180

agatggaaca gggtcgaccg gtcgaccggt cgaccctaga gaaccatcag atgtttccag     240

ggtgccccaa ggacctgaaa tgaccctgtg ccttattga actaaccaat cagttcgctt     300

ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata aagagccca caaccccctca    360

ctcggggcgc cagtcctccg attgactgag tcgcccgggt accgtgtat ccaataaacc      420

ctcttgcagt tgcatccgac ttgtggtctc gctgttcctt gggagggtct cctctgagtg     480

attgactacc cgtcagcggg ggtctttcac tctctgtgta ctggtaccaa cagagcctgg     540

accagggcct ccagttcctc attcagtatt ataatggaga agagagagca aaaggaaaca     600

ttcttgaacg attctccgca caacagttcc ctgacttgca ctctgaacta aacctgagct     660

ctctggagct gggggactca gctttgtat ttctgtgcca gcagcgtagg tggtagcttg      720

aaacagttct tcngggccag gggacncggc tnaccgggnn aggtaagaag ggggcctcca     780

ggtgggaaan aagggtgagc agnccanccc tgcacgaccc nnnaaccntn ttcttagggg     840
```

14

gaggggnnca ctgggncatn ncagggccnt cntngnggaa nnggggtttg cgccnagggt　900

ccccagggct gngc　　　　　　　　　　　　　　　　　　　　　　　914

<210> 21
<211> 1604
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1604)
<223> n is a, g, c, or t

<400> 21
gngtggnatt gtgagcggat aacaatttca cacagnaatt cagtaaatgt tgatgtcaca　60

ttgggggcag cagctctagc tacattcaac tctacctgaa aactggcttt tagtataagc　120

catggatcca taacacatag gctagtttac aacaagtaat ttcagcattt ttggataatt　180

acattccctc cgacaatttc taaggagcct gcatgatact gaactgtgtc agaaaatagg　240

tgctacagtg aatatgtgat tctaatcagg ctttttact atggaattat agtaaaatgc　300

actataatca actcatataa attgctctgt gcctatactt atctctaatg aagggaagca　360

aattgcctta cctgaaatta taaaagaaaa tgattacaaa ggtatggaag tttataggca　420

tcttataaga cctgatttta ttatgcatta tatagatggc aaaaaattcc tatttatcca　480

gaatctaaat gaccaggaag ctcaaataaa atgtgtttca tgggaatttg tttttatgtg　540

ctgaattgca agatcctgaa gggtctttaa gatcatcaaa gaaacatgaa tgctcacaca　600

actttagagc tgtaagaggt gtggagttca catggcccaa cctgtccatt tgacagctgc　660

gtgctgagcc caggggagag catggcttgc ccaatgaatt tgtgacaaag cgagacctgg　720

rgnnaccttt cagtttccct yatacccac aaatgggtct ttgtgctcta ctaggkgnaa　780

tggtattaaa taccacagnc cttttgtgta ttctaantyc ttagaaattt cctaatttat　840

gcatgggycc mcccttgcta aaatttcagc atacaccatg atatcttaga gctcccttcc　900

cacttaatct tctctcttag cattttcacg atttaaaaaa atcatctgta ttccccatta　960

gcaggcaaga ttcctaagga caaataactt ttttctttt attcactgct gaatcaccta　1020

gaacggtacc cagcacaaag tgagaggttg agaaatagtt gttgaatgaa aaaaaaaatg　1080

aatcgtttat gataatcctc aaatcccatc actgcattat cagaataccc cattttttat　1140

gtcatctatt tgacactttt ccagaacttc tgatgtgcca ggcattttac aaggctgagg　1200

tgaaccacag agtaataggc ttattttatt cattcaggga gcttaattta aggtgatcct　1260

attattgtaa cctcctaatg caatgtcatc tcttatcagc ttaattctgc agactgtagc　1320

15

tatgtattac tccctgaagg aattattttc aocttcaacc tgaagttagg actcatgatt   1380

cagcaatctg ctttctggga tcatacaagg gaaattgcaa tctttgtgct tgcttgccaa   1440

agctgagaaa gatggagcag natcaaaata agcaggattt gccaggcaat tttgacatat   1500

tcttcctctc acatataacc atcacaaagt aatgcatttc ataatgagaa ganccttgca   1560

ctagaagcat acatagtatc acatgnctca tcttctngnt tctn   1604

    <210>   22
    <211>   844
    <212>   DNA
    <213>   Homo sapiens

    <220>
    <221>   misc_feature
    <222>   (1)..(844)
    <223>   n is a, g, c, or t

    <400>   22
    ttggggancc gcttgccaaa cnttcaggtg gggtctttca agaggtctcc agacctaggg   60

    gagcatctca gcgtcactcg ctgtccagtt gctgtgatca ggtgctttgg ggtttgtgtg   120

    actccagaat ccactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag   180

    aaagcctcct gctgaagtca tcgttggccc acatgcattt cagggacaag aaatgaagat   240

    cggagacttt caagttgtgc ccaggactca cctgctccca ggagacaaaa ggccacacag   300

    cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctggtgtc tctgtagtaa   360

    gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc   420

    acactgacat actttcccct gcaggccact ccagcccact gtactctttg gcaggcctca   480

    ggttctgcta ctccatgtac tattcctgtc ttgcacaggc cagaagctaa aggtgaggag   540

    ctgccctgac actgattccc cagcccttgc accccagccc cttcaccctc cactgcccgt   660

    gcagcagcag agacactccc tccttgatgc aaactgaggc ctctggcacc cnactctttc   720

    agggcaatga tagtctgtgc ttaactctac atggccaggc cccactcagg gaattcttat   780

    gaaattatta ttttttttnta ttctgggaa acaaagcgat gtattattt ctgtttnggg   840

    gata   844

    <210>   23
    <211>   1562
    <212>   DNA
    <213>   Homo sapiens

    <220>
    <221>   misc_feature

                                    16

<222>   (1)..(1562)
<223>   n is a, g, c, or t

<400>   23
ttttacanaa ctnncccccc tnaatcaaca gaatatacat tttnttnagc cccncaatac   60

acttattcta aantgnccca cataatngga agtaaaccac tcagcaaata taaagancag   120

aaatcccanc aaactgtctc tcagaccaca gtgcaatcaa attagaactc agggttaaga   180

atcacactca aaaccacaca actacatgga aactgaacaa cctgctcctg aatgactact   240

gggtaaataa tgaaatgaag gcagaaataa acacgttctt tgaaaccaac tagaacaaag   300

acacaatgta ccagaatctc tgggacacat ttaaagcagt gtgtagaggg aaatttatag   360

cactaaatgc ccacaagaga aagcaggaga gatctaaaat cgacatccta acatcacaat   420

taaagaact agagaagcaa gagcaaacat attcaaaagc tagcagaaga cgagaaataa   480

ctaagatcag agcagaactg aaggagatag agacacaaaa aaaaccttca aaaattaatg   540

aatgcaggag ctggtttttt gaaaagatca acaaaatagc cctctagcaa gactaataaa   600

ggataaaaga gggaagaatc aaatagatgc aataaaaatg ataaagggga tatcaccacc   660

aatcccmcmg aaatacaaac taccmtcaga gaatactata aacmcctgta tgcaaataaa   720

ctagaaaatc tagaagaagc agataaattc ctggacacat acaacctccc aagactaaac   780

caggaagaag ttgaatctct gaatagacca ataataggtt ctgaaattga ggcaataatt   840

aatagcctac caaccaaraa aagtcgagga ccagatggat tcacagccgt attctaccag   900

aggtacaaag aggagctggt accattcctt ctgaaactat tctgatcaat gagaaaaaag   960

ggaatcctcc ctaactcatt tatgaggcta gcatcatcct gataccaaag cctggcagag   1020

acacaacaaa aaaagaaaat ttcaggccaa tatccctgat gaacattgat gtgaaaatcc   1080

tcaatacaat actggcaaat caaaaagctt atccaccacg atcaagtcag cttcatcgct   1140

gggatgcaag tctggttcaa catatgcaaa tcaataaaca aaatccatca cataaacaga   1200

accaatgaca aaaaccacat gattatctca atagatgcag aaaaggcctt caacaatatt   1260

caacagcctt tcatgctaaa aactcttaat aaactagata ttgatggaac atatctcaac   1320

ataataagag ctatttatga caaacccata gccaatatca tactgaatgg gcaaaaactg   1380

gaagcattcc ctttgaaaac cagcacaaga caaggatgcc ctcttcacc acttcgattc   1440

aacctagtat tggaagttct ggccagggcc atcaagcaag agaaagcaat aaggggtatt   1500

caagtaggaa gagaggggnt ttctgtgtga aaangttanc cgctggnnan ccccaaanan   1560

aa   1562

<210>   24
<211>   1446

<212>   DNA
<213>   Homo sapiens

<220>
<221>   misc_feature
<222>   (1)..(1446)
<223>   n is a, g, c, or t

<400>   24
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gagtcagctg cgcgggcccc cggatoctgg gctgtcatgt aacatcttcc aataaatgtg   120

atcttgggag gagaccattt tgggccttgg tttccacatc tgcgaaatgt tattatagcc   180

atgaacactt actgaaagct taccccatat gccagacaca tcttccaatc aacttatgtg   240

agttatctca tttaattttc acaacaatac aaagtagcgg ggaaaacttc tggcttctct   300

tgaaaactca gaaaatctaa caatgttgag tatgagtcca aaatgtcagc aagaagccag   360

agctgaatag ggaaggctgt tttagatgag accattagcc acagacctca ccactcttct   420

tactgtgcta cttatttcct ttatagtacc tgagtggttc ctgctgcgtg tgggtttgtg   480

gcccctgcat tagatggncc ttnatnattc ctcttcaccc ctgagctttg atgtttttg   540

ctccatgtca ccttcaccag agtggtcagg ccattcttca atattcwkac ctrggcaaaa   600

ggtgcatgac tttgaactcc cctagttaag ttaaggcttc takaawgaac angannangc   660

tttgggagct gaggaagggt gctcactgtg ccctataaaa tagagtttca atagacactg   720

ggtcctctgt ggcctgacct cccctgtgtc agcaacttga gtctcacttg aatggggaaa   780

gaaagtawtg arangaaakg aacwwkgaam ytcwgaaaca ngacctcttm akanswarcm   840

aggrccctms tagtctanyt wrggtaaagc caagtgtgac cctaaggcaa gttacttaac   900

ctctgcgtct cagtttcctc atctataagt taatgacaac ctctacccca taagggagct   960

tgaaagaaaa tccaaaaaag aaagaatctc tttgagttgc taatgactct taagtttctg   1020

gttctagtcc tttgaccatc atgacagtcc tatggtttta cgaaagaact atccatctct   1080

atttaaaaaa caaaaaacac aaagaccttt tttgcttaag ctaacttgtg ttgggtttca   1140

tccaccagga agttagagag agaaattact tagagataaa cttacacatt acaaatcctt   1200

ctgttctgtg tgcttttaaa aatgttcaat ttctaaatgg gcctctggtg aagataatga   1260

tcacctcatt gatttgttcc caggagaaca gggtaaaatg aagtcctgct gatcacattt   1320

tctaaatctt tttantccca ttgctttggg aaagtttcta caccagtnat ccttntacag   1380

cctccctctt tcccatggtt cnttctctgc accaccagga aaggaggaat cccanancag   1440

tcttgc   1446

<210> 25
<211> 840
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(840)
<223> n is a, g, c, or t

<400> 25

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ggaattgnna gcggntaaca atttcacaca gnaattctta ttatggtaag ttcctgagat      60

ttgagatggt ttgttataca acagggaact gataggctta ttcttcaaga ggagcaaaac     120

agggatgatt gctattctct tcaatgggtt gaggaaagaa gaaattatgt gaacatttat     180

acactaataa tttattctgt catatttcag tcagattaaa gcaaacagcc aaaaacaagg     240

acaaagtcca aggtaagaga ctgatgataa gtggcctgtt tacaaggaaa ataagatcac     300

tagctctact tacagctgat tcagaataac ttcattttta aagcctaaaa ttttacagtc     360

aagctcttga gtgcaatttc cttaacattt tctaaaccat acagaaaatc ataaagaaac     420

aatatttctt tgtttgagtt tccttttttag gagttaggtc ttattttaaa aatattttct     480

agcctgttta ggctcttatt taaaattatc tacttttctc aaagtctttc tcatacttga     540

gatatccaaa atattgaatg agtgatgtaa actataccag ataaactatg agtctatatt     600

tttaccctga ttcagtcagt ttccaaggag aactttgaac aactaaaaat gtgtattact     660

ataatctctc tgaaatattn ctnattaatt ttttggggggn aaaatgagtc attctgagcc     720

aaaaaaaaaa anggtnacca gacantttcc actnctaact tgnntgggcg attncagcag     780

attcaanttc cagcatnggn agatncggna gatnnnggnc ctaccatgan cttaccttcc     840
```

<210> 26
<211> 861
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(861)
<223> n is a, g, c, or t

<400> 26

```
ttttnctcct aacttgagtt ggcgatatca gcagattcaa attaccagca atgggaagat      60

acaggaagat gtaggtacct accaatgagc ttaccttccc agtgctctat ataacctcac     120

ttctatagcc caaagtatta aaaagaagaa aaaataataa ttcaggctta ctatttaaaa     180

atacagtgat tctggccggg cacggtggct cacgactgca atcccagcac tttgggaggc     240
```

```
cgaggcgggt ggatcacgtg aggccaggag tttgagacca gcctggccaa tgtggtgaaa    300

ccctgtctcc actaaaaata caaaaattag ctgggcatgg tggcgggcgc ctgtaatccc    360

agctactcgg gaggttgaga tgggagaatt gcttggaccc aggaggcaga gcttgcagtg    420

agccaagatt gcaccactgc attccaccct gggtgacaga gtgagaccct gtctcaaaaa    480

acaaataaaa atacagtgat tctgagaggc cttccctttc cacaccacct cctacttgtt    540

tgatagctct catcccattt tcctcaactg ccacatatgg ccaggacttc cacagtgtat    600

taaacatctt ctttggacaa gagaaatttc actgaagcaa tgagtgtaga agttattagc    660

atgaattgaa gactgatgct ggcacacaaa tagggagaca catcaatata atgacctaat    720

gaatctagaa atagcttcan gaantntgga aaagtagatg tgataaaagn tgcatttnaa    780

tcanngagca aagtnttaat anaattgaga cacctatgtn gctattngga aacattaang    840

tnggntgcat antngaaact t                                              861
```

```
<210>   27
<211>   875
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(875)
<223>   n is a, g, c, or t

<400>   27
ttgggnnacc gcttgccaaa cctacaggtg gggtctttca agaggtctcc agacctaggg    60

gagcatctca gcgtcactcg ctgtccagtt gctgtgatca ggtgctttgg ggtttgtgtg   120

actccagaat ccactgggcc tgtgtgtcag aagacaaaag ttaaccataa ggcacagaag   180

aaagcctcct gctgaagcca tcgttggccc acatgcattt cagggacaag aaannnagat   240

cggagacttt caagttgtgc ccaggactca cctgctccca ggagacaaaa ggccacacag   300

cagaggagcc tgaagcccat ggcaggatct cctagcttgg ggctggtgtc tctgtagtaa   360

gcattctgaa gttcctaagc tcccttcttc ctgataggag cattgacctg tgatgtcacc   420

acactgacat actttcccct gcaggccact ccagcccact gtactctttg gcaggcctca   480

ggttctgcta ctccatgtac tattcctgtc ttgcacaggc cagaagctaa aggtgaggag   540

gactgaacac agtaccaaca tacccacatc acaccttact ttcctctgcc cgccctgtcc   600

ctgccctgac actgattccc cagcccttgc caccccagcc ccttcaccct ccactgcccg   660

tgcagcagca gagacactcc ctccttgatg caaactgagg cctctggcac cccaactctt   720

tcagggcaat gatagtctgt gcttaactct acatggccag gcccccactc agggaattct   780
```

```
aatatgaatg taaactncag gtgttgncag ctagtgcttc cntggaaaan cccctgttnc      840

agctnctaca catgctctta tctntagctn ganca                                 875
```

```
<210>  28
<211>  901
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (1)..(901)
<223>  n is a, g, c, or t

<400>  28
ctncttctng gngtnnnnn nacnatntan nnnnatcgnc tcnacantnn nttncnnggg        60

aaaaacctct gtctaacctt acatgaaaaa acccgtttcc aacgaaggcc tctaagaggc       120

caagatatcc acttgcagac tttacaaaca gagtgtttcc aaactgctga atgaaaagaa       180

aagttaaact ctgtgagttg aacgcacaca tcacagagca gtttctgaga atgattctgt       240

cgggttttta tacgaagata ttcccttttc tgcctttggc ctcaaagcgc ttgaagtctc       300

cacttgcaaa ttgcagaaaa agagtgtttc gaatctgctc tgtctaaaag aaggttcaac       360

tctgtcagtt gaatacacac aacacaagga agttactgag atttcttctg tctagcctta      420

catgaaaaaa acccgtttcc aacgaaggcc tcaaagaggt caaaatatcc acgtgcagac      480

tttccaaaca gagtgtttcc aaactgctga atgaaaagaa aagttaaact ctgtgagttg      540

aacgcacaca tcccagagca gtttctgaga aagattctgt ctagttttta taggaaaata      600

tttccttttc tgcttttggc ctcaaagtgc ttgaaatctc cacttgcaaa ttccacaaaa      660

agagtgtttc aaatctgctc tgtctaaagg aaggttgaac tctgtgagtt gcatacacac      720

aacacaaaga agttactgag aaatcttctg tctagcataa tatgaagaaa tcccgtttcc      780

acgaaggcct caagaggncc aatatncact ggcaggcttn caacagagtg ttnctactgc      840

tctgtgaaag aangntaact ttgnngttga ccaccatnan aagnnttttg naanatttgn .     900

n                                                                      901
```

```
<210>  29
<211>  856
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (1)..(856)
<223>  n is a, g, c, or t
```

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<400>  29
cntttggnng tttaaaangg gcnganatat gcttnacatc nattgggggn aaacctcttg      60

cgtgagtatt caagaaccct ctcttgggat ctggatcggg acccctttcc tgtaacatat     120

gcaaggaaag aaatgcagag gaatggaact gagccatgga acagacattt ggggttgggc     180

aggaggagtt agcagagaga tctgcatagc tcttatccta cttagcacta gtgctgttca     240

aggtagaact cacagcataa gaattctagc atctgcataa atttggagag caacttgcct     300

tctccttaga tacacgaata tggaaaatgc aatagaagtt gcttatcatg cactcaggtt     360

gagtgaagtt ttatcataat gaagctaaat gaaattccca aattgctctg gtggagagga     420

acgccttgat attccacttg tggaaaaatg gctctatgcc aaaaataaag ttacatcaac     480

ctcagtacag gagaaatcag agtttctgct cacagcagca gcagaggaat catctgcaac     540

acagagactt ttgggttgta tgtaaggcag ccttgctgga tggtctttaa cagggttttg     600

gtagggacat ggtagaggct ggttcctaaa ctcttcaaac gtttcttccc agcccttag     660

ctttgacctc acgtgcagag ttgagttaat tataagcctt atttatgggc acactttcac     720

cattaagttc atacacagcc ccattttgt gccattcttc actcctatgt cctttctcc     780

cctaagcaac catgtaaaca tgttagagng ggngagcgtg cacacnccat acacacacat     840

tcatttacac atgatt                                                     856
```

```
<210>  30
<211>  890
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (1)..(890)
<223>  n is a, g, c, or t

<400>  30
cnnnttctgg gggngtannn aactaannna nntnaatncc ncccaatnnn ttcggggggg      60

aaaancccca gnactccata attcncaagn atcacatgna tcacaggaga ggagactggg     120

ggagtcaatg gatagaggat ttataagcca agaaaaaaaa atggagcccc aaactgtgaa     180

atccaagaag ggggtcatgt gaaccccaat ttatagccag tttttcagaa gaataagtga     240

caacctacta cttgtgattg gcacttgaag tgggaggcag tcgtgaggga gttaatatgt     300

gggaactaac cctactctag gtagtgttga attgaatcaa atcataggac atctagttgg     360

tgtttgctgg aaaactggtt gttggtggag tgaaacccct acatattttg gtgatcagag     420

gtgaagtgtt gtgttaagtg gtatgagact gggaaaaaca ctttggtttt tcctgtctct     480

cacagaatta aagtttccaa gagaagcatc agaagagtgg aaggttggga ccagcaaacc     540
```

```
acaagcccta ggccccaaac tagggtcaag tggaaaagca gggtataata gtgaaatggc      600

cctcctctcc acttctgcag ctccagtgac gctgttccta ctcattgtca cactggaatg      660

gttgcaggat gaacacgatc ctctggaaat ggagacatct tctgaaggta gaggaaactg      720

cagtcttcct gcccccgacc gccactcgca gaggttggga atgtcagcct nctccaaccc      780

antctttnt atgggatttt ccttactttg ggggggact gnaatgntac ctatctttt       840

tttacaantt ggggggggntc cncccactt anngacccng nttnnccnng              890
```

```
<210>   31
<211>   732
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(732)
<223>   n is a, g, c, or t

<400>   31
attctttggg gnaccgtcag naccaagttt tactcatatc ggcatcctct ctcggtggct      60

gctgcagcgg ggctggtgtg ctgcaacccg dacggagctg agtgaggggc acaatggcag     120

caacctgcag gcaccaaaga gcccccaaga gctgctcagc ggtgcctgat caaagtttgt     180

ctgggccagt gcttgtgcat tgtgtacgct gtgcgacaac caggaaggag agctgggttt     240

tgccatcctc caacgcttct taaataggaa acttttnggg tagcacctgg cctagttcct     300

ggaacacaga aggtgctgag tgatgttagt ttcattcgct catcttgtct cttgggcatg     360

gaaaagagtt tacaagtgct ctttcattat ccatcttgat gtgggaaggt ggggcagggg     420

aagatgagta cccgctctcg ccctttggtg tgatgtttgt dacgtacatg aggcatgtgg     480

gagagtggat cacagcattg gacagactgg atccttctg gtcccacatc actcaggcaa     540

ctctctcttc ccacctgccc cccaaactcc cttncacctc cctccacatg tatcctccca     600

cttncttcca ctcatgtaat gagaggtgct gatgagtcac aggaagaggt agccctagat     660

aaccaacaga ctgcaaaacg ggacagtncc ntggatgtct gagccagtgt ttngngcact     720

gcattgactg gc                                                       732
```

```
<210>   32
<211>   672
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
```

```
<222>   (1)..(672)
<223>   n is a, g, c, or t

<400>  32
tttggnaacc gtcagaccaa gtttactcat atcggatccc aggagacacg ctccaagggc       60

tgggtgggaa aagccccaga aaggggaggg ctgcggggag tgagaatcgg gatggacctc      120

acagacgaca aacagatgga caaaaagctt ctctccctgc cgctccctcc ccgccaccaa      180

ctccagcccc tctgtctcca tccccttttc ctgtctgtcc tgtctgaatc tctgaatctc      240

tgcctgtttn tttttctctc tatgaatcac agcgtttcag agcctctgag agaaaaatgg      300

gaaaagaaga cagagatgat agaaaatgca gagtgtgcgt gtgtgtgtgt gtgtgtgcat      360

gtgtatgcgc gcgtgtgtgt gtgtgtctgt gcatgcgtgc acccagcatg aagtctggtc      420

tggagaatgt aactagggag ggaggaagag aggggacgag agaagcagag gatgaacaaa      480

gagactttcg aagctcatag gaaaaagcct gggaggcaac agcagcaggg acacgcatat      540

gccgcacacc cctacacaca ccacacacca cacaccacac acaccctgca tgcaccctgg      600

agacatgccc cagactccag gcgggagggg tggagcaggg ggtgtgaaat atggttggtt      660

gggttgggtt tg                                                          672



<210>   33
<211>   770
<212>   DNA
<213>   Homo sapiens


<220>
<221>   misc_feature
<222>   (1)..(770)
<223>   n is a, g, c, or t

<400>  33
nttttgnant gtncgcggnt aacaatttca cacagnaatt cattttaacg ttgtacatat       60

ttattataca agaaatattt tttccatcaa aaagtactca ttcaaaaaat atttaatcta      120

gaatagagat tataaatttt taacttaatt ttattttttt cttaaggaaa actctaagat      180

atcattacca ttttcaaaac tgtcaagtag tggtgaatga cacttcttat atgttaattt      240

ttaaaagaat atttctaaca cacattctta atggagaatt atatcttata cagaatgata      300

cattctaagg gtgatgttta tgaaagaaat ttaagcttgg ttaacatgct tagtaaaatt      360

ttttaataca aataaaattc agagtatatg gtgtgaagtg agttatatgg tgcaaatact      420

attttaattc ttgaacactt ccacaaaatt agcttgtaaa ataaaattaa acccacactg      480

agatgctaga tttgcagatg aatcattcat tttttttacat ttcttttttat ttctctaact      540

aaattatatg acagaaggca agggtcatga ttaattcatt gttgtattct ttatatatta      600
```

```
aatataagct cctcaataaa tattatggaa aaaatgaaca aacacttcac attttattgt      660

tttctatatt tttcaaggtt tttattaatt cttcatgtgc tttgtgactt tattttctcc      720

aaagaaattc ttcttgaaat gaaaagttca caanagttag gataactgga              770
```

```
<210>  34
<211>  777
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (1)..(777)
<223>  n is a, g, c, or t

<400>  34
nttttgnatt gtngcgcggn taacaatttt cacacagnaa ttcttttgtc aagaattata       60

agaagaaatc ccgtttccaa cgaaggcctc aaagagttcc aaatatccac ttgcacactg      120

cacaaactaa gtcttccaa actgctctat gcaaagaaat gttcaactct gtgagtttaa      180

tacacacatc acaaagcagt ttctgagaat gatactgtct agtttttata cgaagatatt      240

tccttttgta ccattggcct catactgcta gaattttcca cttgcaaatt ccacaaaaag      300

agtgtttcca atccgctctg tctaaaggaa ggttcaactc tctgatttga atacatacat      360


caatataaaa cgtagattgt cacttcaaga aaatacctgc cttatacaga actaagtggc      480

tgtttcaagt aaaaatggtg ttccatgaaa aagctgctag ttcagctggc aactcaaaca      540

atggcacaag tgccttatgc catttctatt ttatcacaca tattaaaaac ctggccagca      600

cggtggctca tgcctgtaat tccagcattt tggnaaggcc gaggcaggtg gatcatttga      660

ggccagnagt tcaagacang cctggccaac atagcaaaac ccccattttt actaaaatac      720

aaaattagcc aggcntgggg gcgcgtgcct gtantccnnc ttctcgggag gctgagg       777
```

```
<210>  35
<211>  799
<212>  DNA
<213>  Homo sapiens


<220>
<221>  misc_feature
<222>  (1)..(799)
<223>  n is a, g, c, or t

<400>  35
tnnttttgga gtgancgcgg ntaacaattt tacacaggaa ttctagggtt ggttcatggt       60

ttgagacttg agagtggaca ggtgcctagt tagacctgct ctggatgtgg aggtgtctgg      120
```

25

```
tgattagaat gactctttgt atatctgttc cctcttaat tgcttccttt taacctcaag      180

attaggcttt tattgcataa taaaatgcat atgagccatt cagttttact ccattacctc      240

tctggcttag aatgaactat cagtagaatt aacaaaaatt gcatcataga gttggagaat      300

tgccaccaag gaagtgttct agccatacta cagaaaagat tctccccatg ggattacttc      360

tcagtagaat tcagcaacca attcctggtg aatctatcca agcagagaaa tgaaaacata      420

tattcactaa aagacttgaa cacaaatgct catagcagcc ttaatcaaaa tagagaaaaa      480

ctggaaacat ttcaaatgtc tatcaactga tcaatatata agcaaaatat ataaagcatt      540

tgcagacaat aaaaaacaaa atattgatat atactaaaac atggnatgaa cctcaaagcc      600

actatactag atgagagatg tcagacacaa acctactgta tttgcaagat gccatttact      660

tgaaaaatcc agaaaagtcg catttacaga gacagtaaaa cagataagtg ggctgcctgc      720

ggctggggggg ttgnaaaagc nattttgctg caaatgaact tanggaaatt tttttttgngg      780

ggggggngat anaaaattn                                                   799
```

```
<210>  36
<211>  417
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(417)
<223>  n is a, g, c, or t

<400>  36
ancttggtaa ctgtcagnac caagatttac tcatatcgga tccccaggaa tactattctt       60

taaagactat caatattcta caaagggaaa ttagagttct caattgtgaa cggaaaggaa      120

catcaatggg catgacctaa gacctccttc tacacagtta aacaacaatt tcacaagata      180

tgatttaaga gaaagctttc agggacgcct gggtggctca gtggttgagc gtctgccttc      240

cgctcagggt gtgatcctgg agttccggga ctgagtcccc atggggctcc ctgcatggag      300

cctgcttctc cctctgccta tgtctctgcc tctctctgtg tctcatgaat aaataaataa      360

agnncttatt tttttaaga ttntatttat ttatncatga nagagagaga gaggcng          417
```

```
<210>  37
<211>  434
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(434)
```

26

<223> n is a, g, c, or t

<400> 37

```
tggtaactcg tcagnaccaa gatttactca tatcggcatc cccaggaata ctattctta      60

aagactatca atattctaca aagggaaatt agagttctca attgtgaacg gaaaggaaca     120

tcaatgggca tgacctaaga cctccttcta cacagttaaa caacaatttc acaagatatg     180

atttaagaga aagctttcag ggacgcctgg gtggctcagt ggttgagcgt ctgccttccg     240

ctcagggtgt gatcctggag ttccgggact gagtcccaca tggggctccc tgcatggagc     300

ctgcttctcc ctctgcctat gtctctgcct ctctctgtgt ctcatgaata aataaataaa     360

gtccttattt tttttaagat tttatttatt tattcatgag agagagagag agncngngnc     420

ntnggcngng ggng                                                      434
```

.<210> 38
.<211> 1425
.<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(1425)
<223> n is a, g, c, or t

<400> 38

```
cnggncggng angattntng tcgnnaccca tggcgaatgc ctggctngcc gaatattcat      60

ggtggaaaat ggccngcttt tctggattca tcgnactgtg nccggctggg tgtggcggac     120

ccgctatnca gnacatagcg ttgggctacc cngtgataat gctgaagagc ttggcggncg     180

aatgggctga ccgcttcctc gtgskkkanc ggtatcgccg ctcyccgatt cgcagcgcat     240

cgccttctat cgccttcttg acgagttctt ctgagcggga ctnctggggt tcgaaatgag     300

ctagccctta agtaacgcca ttttgcaagg catggaaaaa tacataactg agaatagaaa     360

agttcatctc tgctgtcttt ggccattctc tctaggcatc tgctcatgtg gaggcataag     420

aaaatattga catgcttcac attacatttt cagagtatgt tattcatgta atttatttgt     480

aaaatctacc aatacaattt cccccaatc aagtaaaact aggtaaaaag atctctgcaa     540

agattagctg aggaagaaac atatgtgagt agaatcagaa tgttaagagc tgacaggtta     600

gcagatagca tgcccatgat ttttgtgggt ttggcccctt tgttgaagct aaatcttaca     660

gagaggccca accctagagg taaaatgatt aaaacagatg tgctgcagtt ggcggggagg     720

gtgctgcgcc aggggaagcc caagactgct gctggctgcc ttccctcctg aycttatccc     780

atgtctcatt tgaaaaccaa tagttgaaaa actctcaatt ttcagatgag aacgaaaaca     840

aaaatgcaaa gaaggcaaat gattcaytca aarwtactca gtgaatkrga sccawsatgt     900
```

```
gggaatacaa ctctggcctt ctgtttctga atctagtggt atttccaggc tcacaggaag    960

cttcctgtac cttgctccac tgtgtgtgtt tttggatggc cctggtgttt gattacctyt   1020

cgtggcaggc ccaacagccc ttgctaaggc acagactgca tatttgctga tccctgaggn   1080

ggaaagctgt gattcagact ttgaggtcta agaattgcag acttagtttc tagtctccg    1140

atgaaactgc taatctgggt gccagtggtg tttctgctac acggacacct gcccacacag   1200

catgattaga aattataatg atgacggcga tgagtcttcc aggacaccta cgttctttgc    1260

aagatatttc tgctaatcgt ctctaccaga atcagttgga gaactttttt tagttttttt   1320

tttttttttt taatttcccc ctttctaagt caagtaaaaa tactagttta attnctggtg   1380

tagggtaatg atttgtcctc accattactg atgtgtcatt ttttg                   1425
```

```
<210>  39
<211>  674
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(674)
<223>  n is a, g, c, or t

<400>  39
caaaaaatga cacatcagta atggtgagga caaatcatta ccctacacca gnaattaaac     60

tagtattttt acttgactta gaaggggga aattaaaaaa aaaaaaaaa aactaaaaaa     120

agttctccaa ctgattctgg tagagacgat tagcagaaat atcttgcaaa gaacgtaggt    180

gtcctggaag actcatcgcc gtcatcatta taatttctaa tcatgctgtg tgggcaggtg    240

tccgtgtagc agaaacacca ctggcaccca gattagcagt ttcatcggga gactagaaac    300

taagtctgca attcttagac ctcaaagtct gaatcacagc tttcccctca gggatcagca    360

aatatgcagt ctgtgcctta gcaagggctg ttgggcctgc cacgagaggt aatcaaacac    420

cagggccatc caaaaacaca cacagtggag caaggtacag gaagcttcct gtgagcctgg    480

aaataccact agattcagaa acagaaggcc agagttgtat tcccacatga tggctctaat    540

tcactgagta actttgaatg aatcatttgc cttctttgca tttttgtttt cgttctcatc    600

tgaaaattga gagtttttca actattggtt ttcaaatgag acatgggata agatcaggag    660

ggaaggcagc cagc                                                    674
```

```
<210>  40
<211>  666
<212>  DNA
<213>  Canis familiaris
```

<220>
<221> misc_feature
<222> (1)..(666)
<223> n is a, g, c, or t

<400> 40
cccatgagca aaaaatgaca catcagtaat ggtgaggaca aatcattacc ctacaccagn   60

aattaaacta gtatttttac ttgacttaga aaggggaaa ttaaaaaaaa aaaaaaaaaa   120

ctaaaaaaag ttctccaact gattctggta gagacgatta gcagaaatat cttgcaaaga   180

acgtaggtgt cctggaagac tcatcgccgt catcattata atttctaatc atgctgtgtg   240

ggcaggtgtc cgtgtagcag aaacaccact ggcacccaga ttagcagttt catcgggaga   300

ctagaaacta agtctgcaat tcttagacct caaagtctga atcacagctt tcccctcagg   360

gatcagcaaa tatgcagtct gtgccttagc aagggctgtt gggcctgcca cgagaggtaa   420

tcaaacacca gggccatcca aaaacacaca cagtggagca aggtacagga agcttcctgt   480

gagcctggaa ataccactag attcagaaac agaaggccag agttgtattc ccacatgatg   540

gctctaattc actgagtaac tttgaatgaa tcatttgcct tctttgcatt tttgttttcg   600

ttctcatctg aaaattgaga gtttttcaac tattggtttt caaatgagac atgggataag   660

atcagg   666

<210> 41
<211> 603
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(603)
<223> n is a, g, c, or t

<400> 41
cccatgagca aaaaatgaca catcagtaat ggtgaggaca aatcattacc ctacaccaga   60

attaaactag tatttttact tgacttagaa aggggaaat taaaaaaaaa aaaaaaaaac   120

taaaaaaagt tctccaactg attctggtag agacgattag cagaaatatc ttgcaaagaa   180

cgtaggtgtc ctggaagact catcgccgtc atcattataa tttctaatca tgctgtgtgg   240

gcaggtgtcc gtgtagcaga aacaccactg gcacccagat tagcagtttc atcgggagac   300

tagaaactaa gtctgcaatt cttagacctc aaagtctgaa tcacagcttt cccctcaggg   360

atcagcaaat atgcagtctg tgccttagca agggctgttg ggcctgccac gagaggtaat   420

caaacaccag ggccatccaa aaacacacac agtggagcaa ggtacaggaa gcttcctgtg   480

agcctggaaa taccactaga ttcagaaaca gaaggccaga gttgtattcc cacatgatgg   540

ctctaattca ctgagtaact ttgaatgaat cattgcctt ctttgcattt ttgttttcgt   600

tct   603

<210> 42
<211> 749
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(749)
<223> n is a, g, c, or t

<400> 42
ggtnactgtn cgnaccagtt tactncatat ncggntnccc atgagcaaaa aatgacacat   60

cagtaatggt gaggacaaat cattacccta caccagnaat taaactagta tttttacttg   120

acttagaaag ggggaaatta aaaaaaaaaa aaaaaaacta aaaaagttc tccaactgat   180

tctggtagag acgattagca gaaatatctt gcaaagaacg taggtgtcct ggaagactca   240

tcgccgtcat cattataatt tctaatcatg ctgtgtgggc aggtgtccgt gtagcagaaa   300

caccactggc acccagatta gcagtttcat cgggagacta gaaactaagt ctgcaattct   360

tagacctcaa agtctgaatc acagctttcc cctcagggat cagcaaatat gcagtctgtg   420

ccttagcaag ggctgttggg cctgccacga gaggtaatca aacaccaggg ccatccaaaa   480

acacacacag tggagcaagg tacaggaagc ttcctgtgag cctggaaata ccactagatt   540

cagaaacaga aggccagagt tgtattccca catgatggct ctaattcact gagtaacttt   600

gaatgaatca tttgccttct ttgcattttt gttttcgttc tcatctgaaa attgagagtt   660

tttcaactat tggttttcaa atgagacatg ggataagatc aggagggaag gcagccagca   720

gcagtcttgg gcttcccctg gcgcagcac   749

<210> 43
<211> 1778
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(1778)
<223> n is a, g, c, or t

<400> 43
gkggtagngn rcggtaaaca atttncacac agcaattncc cctgtgnaaa ctgccttgac   60

ttggtgcctt ttttggaggg gtggagttgt ttccactttg acaaattttt atattctcc   120

.30

catcctaatt ggactaattt gctttatat ctcttctgtg gttattttgt taatcgtatt   180

ttaggaaagt cacctatttc aaattgattt gcatggagct aaataatttc ttccaatttt   240

ttcattccct ttgtgtttat ggttatttct acattattag tgaaagtttt gtggttttgt   300

gttttagttc tctatctcct cttttgatta gtttcacaga gtttagttgt tattttttca   360

gaaaacagct cttgcactta tttatcggct ctactgttct taatttgctc ctaaaaattg   420

tcaataatat gtttcttttg ctttgcccgg gctcattttg ttgtttttct aattgtttga   480

gcttgactct taattcatct attttgtttt ctgctttttt gttaatgtaa atttaaaaaa   540

tgcgagatcc aattagaata agcctcaccg gacaagaacc tgtctgtgca cttcgagact   600

accataatgc ctatcacata gcaggtgctt aagcaaaatt tttgtatgaa taaataaacc   660

cctatgaaat aattatggga tttgtgtgac agccctcgtt cttctctgct gtctttggsc   ,720

aytctctcta ggcatctgct catgtggagg cataagaaaa tattgacatg cttcacatta   780

cattttcaga gtatgttatt catgtattta tttgtaaaat ctaccaatac aatttccccc   840

caatcaagta aaactaggta aaaagatctc tgcaaagatt agctgaggaa gaaacatatg   900

tgagtaraat caraatgtta agagctrmca ggttarcaga tagcatgccc atgattttg   960

tgggkttggc ccctttgttg aagctaaatc ttacagagag gcccaaccct agaggtaaaa   1020

tgattaaaac agatgtgctg cagttggcgg ggagggtgct gcgccarggg aagncccaag   1080

actgctgctg gctgccttcc ctccntgatc ttatcccatg tctcatttga aaaccaatag   1140

ttgaaaaact ctcaattttc agatgagaac gaaaacaaaa atgcaaagaa ggcaaatgat   1200

tcattcaaag ttactcagtg aattagagcc atcatgtggg aatacaactc tggccttctg   1260

tttctgaatc tagtggtatt tccaggctca caggaagctt cctgtacctt gctccactgt   1320

gtgtgttttt ggatggccct ggtgtttgat tacctctcgt ggcaggccca acagcccttg   1380

ctaaggcaca gactgcatat ttgctgatcc ctgaggggaa agctgtgatt cagactttga   1440

ggtctaagaa ttgcagactt agtttctagt ctcccgatga aactgctaat ctgggtgcca   1500

gtggtgtttc tgctacacgg acacctgccc acacagcatg attagaaatt ataatgatga   1560

cggcgatgag tcttccagra cacctacgtt ctttgcaaga watttctgct aatcgnttnc   1620

tctaccagaa tcagttggag aacttttttt agtttttttt tttttttttt aatttccccc   1680

tttctaagtc aagtaaaaat actagtttaa ttctggtgta gggtaatgat ttgtcctcac   1740

cattacttga aagaccccac ctgtaggttg gcaagcgg   1778

<210>   44
<211>   868
<212>   DNA

                                    31

<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(868)
<223> n is a, g, c, or t

<400> 44
ttcctgagac ngcttgccaa acctacaggt ggggtctttc aagtaatggt gaggacaaat   60

cattacccta caccagaatt aaactagtat ttttacttga cttagaaagg gggaaattaa   120

aaaaaaaaaa aaaaaactaa aaaagttct ccaactgatt ctggtagaga cgattagcag   180

aaatatcttg caaagaacgt aggtgtcctg gaagactcat cgccgtcatc attataattt   240

ctaatcatgc tgtgtgggca ggtgtccgtg tagcagaaac accactggca cccagattag   300

cagtttcatc gggagactag aaactaagtc tgcaattctt agacctcaaa gtctgaatca   360

cagctttccc ctcagggatc agcaaatatg cagtctgtgc cttagcaagg gctgttgggc   420

ctgccacgag aggtaatcaa acaccagggc catccaaaaa cacacacagt ggagcaaggt   480

acaggaagct tcctgtgagc ctggaaatac cactagattc agaaacagaa ggccagagtt   540

gtattcccac atgatggctc taattcactg agtaactttg aatgaatcat ttgccttctt .   600

tgcatttttg ttttcgttct catctgaaaa ttgagagttt ttcaactatt ggttttcaaa   660

tgagacatgg gataagatca ggagggaagg cagccagcag cagtcttggg cttccctggc   720

gcagcaccnt cccgccaact gcagcacatc tgtttaatca tttaacctct aggntgggcc   780

tttctgtaag atttagcttn acaangggcc aaacccaaaa aatcatgggc atgcttctgc   840

                                                                        868
tacctgncan tntaacattt gattntac

<210> 45
<211> 1237
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(1237)
<223> n is a, g, c, or t

<400> 45
ggtatcgccg ctcccgattc gcaccgcatc gccttctatc gccttcttga cgagttcttc   60

tgagcgggac tctggggttc gaaatgagct agcccttaag taacgccatt ttgcaaggca   120

tggaaaaata cataactgag aatagaaaag ttcatctctg ctgtctttgg ccattctctc   180

taggcatctg ctcatgtgga ggcataagaa aatattgaca tgcttcacat tacatttca   240

gagtatgtta ttcatgtatt tatttgtaaa atctaccaat acaatttccc cccaatcaag   300

```
taaaactagg taaaaagatc tctgcaaaga ttagctgagg aagaaacata tgtgagtaga    360

atcagaatgt taagagctga caggttagca gatagcatgc ccatgatttt tgtgggtttg    420

gccccttttgt tgaagctaaa tcttacagag aggcccaacc ctagaggtaa aatgattaaa    480

acagatgtgc tgcagttggc ggggagggtg ctgcgccagg ggaagcccaa gactgctgct    540

ggctgccttc cctcctgatc ttatccccat gtctcatttg aaaaaccaat agttgaaaaa    600

ctctcaattt tcagatgaga acgaaaacaa aaatgcaaag aaggcaaatg attcattcaa    660

agttactcag tgaattagag ccatcatgtg ggaatacaac tctggccttc tgtttctgaa    720

tctagtggta tttccaggct cacaggaagc ttcctgtacc ttgctccact gtgtgtgttt    780

ttggatggcc ctggtgtttg attacctctc gtggcaggcc caacagccct tgctaaggca    840

cagactgcat atttgctgat ccctgagggg aaagctgtga ttcagacttt gaggtctaag    900

aattgcagac ttagtttcta gtctcccgat gaaactgcta atctgggtgc cagtggtgtt    960

tctgctacac ggacacctgc ccacacagca tgattagaaa ttataatgat gacggcgatg   1020

agtcttccag gacacctacg ttctttgcaa gatatttctg ctaatcgtct ctaccagaat   1080

cagttggaga actttttta gtttttttt tttttttta atttcccct ttctaagtca     1140

agtaaaaata ctagtttaat tctggtgtag ggtaatgatt tgtcctcacc attactgatg   1200

tgtcattttt tgctcatggg atccgatatg agtaaac                           1237
```

```
<211> 703
<212> DNA
<213> Canis familiaris


<220>
<221> misc_feature
<222> (1)..(703)
<223> n is a, g, c, or t

<400> 46
ccctgtgaaa ctgccttgac ttggtgcctt ttttggaggg gtggagttgt ttccactttg     60

acaaattttt atatttctcc catcctaatt ggactaattt gcttttatat ctcttctgtg    120

gttattttgt taatcgtatt ttaggaaagt cacctatttc aaattgattt gcatggagct    180

aaataatttc ttccaatttt ttcatttcct ttgtgtttat ggttattttct acattattag    240

tgaaagtttt gtggttttgt gttttagttc tctatctcct cttttgatta gtttcacaga    300

gtttagttgt tattttttca gaaaacagct cttgcactta tttatcggct ctactgttct    360

taatttgctc ctaaaaattg tcaataatat gtttcttttg ctttgcccgg gctcatttttg    420

ttgttttct aattgtttga gcttgactct taattcatct attttttgttt ctgctttttt    480
```

```
gttaatgtaa atttaaaaaa tgcgagatcc aattagaata agcctcaccg gacaagaacc      540

tgtctgtgca cttcgagact accataatgc ctatcacata gcaggtgctt aagcaaaatt      600

tttgtatgaa taaataaacc cctatgaaaa aattatggga tttgtgtgac agccctcgtt      660

cttctctgct gnctttggcc attctctcta ggcatctgct cat                        703
```

```
<210>  47
<211>  304
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(304)
<223>  n is a, g, c, or t


<400>  47
ctagcttgcc aaacctacag gtggggtctt tcaagtaatg gtgaggacaa atcattaccc      60

tacaccagaa ttaaactagt atttttactt gacttagaaa gggggaaatt aaaaaaaaaa      120

aaaaaaaact aaaaaaagtt ctccaactga ttctggtaga gacgattagc agaaatatct      180

tgcaaagaac gtaggtgtcc tggaagactc atcgccgtca tcattataat ttctaatcat      240

gctgtgtggg caggtgtccg tgtagcagaa acaccactgg nccccagat nagagttttc       300

ttgg                                                                   304
```

```
<210>  48
<211>  735
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(735)
<223>  n is a, g, c, or t

<400>  48
agcttgccaa acctacaggt ggggtctttc aagtaatggt gaggacaaat cattaccta       60

caccagaatt aaactagtat ttttacttga cttagaaagg gggaaattaa aaaaaaaaa      120

aaaaaactaa aaaagttct ccaactgatt ctggtagaga cgattagcag aaatatcttg       180

caaagaacgt aggtgtcctg gaagactcat cgccgtcatc attataattt ctaatcatgc      240

tgtgtgggca ggtgtccgtg tagcagaaac accactggca cccagattag cagtttcatc      300

gggagactag aaactaagtc tgcaattctt agacctcaaa gtctgaatca cagctttccc      360

ctcagggatc agcaaatatg cagtctgtgc cttagcaagg gctgttgggc ctgccacgag      420

aggtaatcaa acaccagggc catccaaaaa cacacacagt ggagcaaggt acaggaagct      480
```

```
tcctgtgagc ctggaaatac cactagattc agaaacagaa ggccagagtt gtattcccac      540

atgatggctc taattcactg agtaactttg aatgaatcat ttgccttctt tgcatttttg      600

ttttcgttct catctgaaaa ttgagagttt ttcaactatt ggttttcaaa tgagacatgg      660

gataagatca ggagggaagg cagccagcag cagtcttggg ctttccctgg cgcaaaaccn      720

tccccgcaac tggag                                                       735
```

```
<210>  49
<211>  1412
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(1412)
<223>  n is a, g, c, or t

<400>  49
cttcccacct nnnacccntg gnccttaaca gncacnnncc tttggagata gctaactcct       60

acncattcaa catcagtgnn anggntctcc tccagaaggc ttcctcnacc ctttcaattc      120

ccacttacnt gtaagcctag gatgcctcct ctcagattca gactggttgn cncagtgttt      180

aagaacttna gctgtacagc canagagttt gtattggaaa ataatctctg tggtttttg      240

tcngcatgat cttggacgag ttatttaacc ccctcagtnt agtttcttca tccatataat      300

ctggcaaatg atagtncnca gtccatacaa ttgtnagcac taaacaaaat aatgtacacg      360

agcctggcac actgaaggan cccagtgaaa ggtggttgtg attactnaca gtccttctca      420

ttctctagca tagcacttac cgtgttgcgt tccgattttc tgtctgcatg tctacctgca      480

tgtcggtttg catgcagact atgaactgga agctgaatcc ccagtgcctg gtacaatgtg      540

agaccccata ncagttcatt gaatgaattc agacacttca gttttttccat aaatttcagc      600

cttcttcaat attttgctcc tattttctag aagtttctga aagagcagct tggaatatgt      660

cagcaatttc taatttctta gcttttcagt gtgtgtgcgc gtgtgtgcgt gtgtgtttga      720

tattttctgc tgtggaaacc gctggactta gatgatcagn ctgtgagata caggcaggac      780

anagataaga agtaggagga gggctncgat gatgaagctt aggcactgaa gcaactcagc      840

cacccaccag gaagcctcag tnccctgaar aggtggaccc tkkcasscyg wggtgaacca      900

ttgtgggcca aagaggccca gtgcatgcat gaggcagacc tccctctaca gggaggcttt      960

gccctactgg gatttatttc cttgctgctt aaggacctgg ctttgctcct gcctttcctt     1020

gtcccttca tctgattctc tggccttatt ttggccagca gattgcattt gcctgtccag     1080

tttaccatat aaatgcattc tcctcctcat gacctcttct cagcctgctg gtctaaggga     1140
```

ggagctctgt ttcttgatcc tgccctctga ctaaattttc tcttgctgct cttcccttc   1200

ctgatgattc agtacagaca cctgcccaat tccacttttt ctcttcatct ccaattattt   1260

ggtggtcaag actgtttact caaatatgca tctggtttaa tcacgagcca cgactctgac   1320

taaagtagcc tgattatatg gttctttaag ggatagctga ctttcacaaa cctaagaaaa   1380

gttncttaaa gtggtgtnct aagggnccta ca   1412

<210> 50
<211> 866
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c, or t

<400> 50
ttnngggacn gcttgccaaa cctacaggtg gggtctttca agatctgctg acagtgaagc   60

taaatctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc   120

tcttaaacaa tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaatttaa   180

ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc   240

ttggtaggag tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag   300

aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc   360

aggtcttgaa atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt   420

cagtaccaga gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat   480

tccagatacg atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt   540

attttggaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa   600

aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag   660

ttacaataga acaacgatag atctctaagg ggagagtgaa aggacctcaa tttgagaaac   720

gtgaggcagg aaaagtttca aataattata ttcagagtgn tacctaagtt gttacttaaa   780

gacattctct acgtaaaana aacaataagg ccaaatgaag gaatgagagt tatgttatcg   840

cagaaacaan gtaancggnt tntttt   866

<210> 51
<211> 597
<212> DNA
<213> Canis familiaris

```
<220>
<221>  misc_feature
<222>  (1)..(597)
<223>  n is a, g, c, or t

<400>  51
acacagcaat tcattncaat gaactgttat ggggtctcac attgtaccag gcactgggga      60

ttcagcttcc agttcatagt ctgcatgcaa accgacatgc aggtagacat gcagacagaa     120

aatcggaacg caacacggta agtgctatgc tagagaatga gaaggactgt cagtaatcac     180

aaccaccttt cactgggttc cttcagtgtg ccaggctcgt gtacattatt ttgtttagtg     240

ctcacaattg tatggactgt gtactatcat ttgccagatt atatggatga agaaactaga     300

ctgagggggt taaataactc gtccaagatc atgcagacaa aaaaccacag agattatttt     360

ccaatacaaa ctctctggct gtacagctca agttcttaaa cactgggcca accagtctga     420

atctgagagg aggcattcta aggcttacag gtaagtggga attgaaaggg ttgagggaag     480

ccttctggag gagatgccat tacactgaat gttgaatgag taggagttag ctatctccag     540

aggggtagtg gctgtgaagg ggcgaggggt agagggtggg aaggggatga tggaagg       597


<210>  52
<211>  875
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(875)
<223>  n is a, g, c, or t

<400>  52
cgcttgccaa cctacaggtg gggtctttca agatctgctg acagtgaagc taaatctggc      60

ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc tcttaaacaa     120

tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa ggatgcctat     180

tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc ttggtaggag     240

tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag aaaaacatcc     300

ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc aggtcttgaa     360

atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt cagtaccaga     420

gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat tccagatacg     480

atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt attttggaag     540

taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa aatataaaca     600

ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag ttacaataga     660
```

```
acaacgatag atctctaagg ggagagtgaa aggacctcaa tttgagaaac gtgaggcagg    720

aaaagtttca aataattata ttcaagagtg ttacctaagt tgttacttaa agacattttc    780

tacgtaaaat aaacacataa ggccaaanga agggaatgag anttangtta tngcaggana    840

aaaggtaaat cggntttttt ttgtatccat tgcaa                                875
```

```
<210>  53
<211>  612
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(612)
<223>  n is a, g, c, or t


<400>  53
agcggataac aatttcacac agnaattcat tcaatgaact gttatggggt ctcacattgt    60

accaggcact ggggattcag cttccagttc atagtctgca tgcaaaccga catgcaggta    120

gacatgcaga cagaaaatcg gaacgcaaca cggtaagtgc tatgctagag aatgagaagg    180

actgtcagta atcacaacca cctttcactg ggttccttca gtgtgccagg ctcgtgtaca    240

ttattttgtt tagtgctcac aattgtatgg actgtgtact atcatttgcc agattatatg    300

gatgaagaaa ctagactgag ggggttaaat aactcgtcca agatcatgca gacaaaaaac    360

cacagagatt attttccaat acaaactctc tggctgtaca gctcaagttc ttaaacactg    420

ggccaaccag tctgaatctg agaggaggca ttctaaggct tacaggtaag tgggaattga    480

aagggttgag ggaagccttc tggaggagat gccattacac tgaatgttga atgagtagga    540

gttagctatc tccagagggg tagtggctgt gaagggggcga ggggtagagg gtggnaaggg    600

atgatngaaa gg                                                        612
```

```
<210>  54
<211>  732
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(732)
<223>  n is a, g, c, or t

<400>  54
agcttgccaa acctacaggt ggggtctttc aagatctgct gacagtgaag ctaaatctgg    60

cggaagcaaa ggattcactt tctcataatg gattaactca tcctatttgc ctcttaaaca    120

atgggtattt taaagacaga agttgaagga agtccaagta tccaatttta aggatgccta    180
```

```
ttagagcagt tataagagag tgtctctctt tctctctctt ctttctttct cttggtagga    240

gtatgcagga ggtcatttaa aagccagata gtgatacaaa tcacaatgca gaaaaacatc    300

cccgtggact cctccctgtc ctatgtttga cattcttaaa atctatgtcc caggtcttga    360

aatctttaaa taatctacca tgttctttgg cctgccctgg gaaatctatt tcagtaccag    420

agctatgctg gttacacacc ttttctgact catgttcnca agtgatttta ttccagatac    480

gatttgggga cagttacgtg tactgttctg atatcttcct aaaaggaaat tattttggaa    540

gtaaagtcac tgataaaatc aactcaggaa aatgcacttt gtaaatatta aaatataaac    600

attattaaag gccatgctgt aaaaaactaa ttgattttcc tgtgtagcag ttacaataga    660

acacgatgat ctctaagggg agagtgaaag gaccttattt ggtaaccgtg aggcagnaaa    720

gtttcaaata tt                                                        732
```

```
<210>    55
<211>    697
<212>    DNA
<213>    Canis familiaris


<220>
<221>    misc_feature
<222>    (1)..(697)
<223>    n is a, g, c, or t

<400>    55
ctagcttgcc aaacctacag gtggggtctt tcaagatctg ctgacagtga agctaaatct     60

ggcggaagca aaggattcac tttctcataa tggattaact catcctattt gcctcttaaa    120

caatgggtat tttaaagaca gaagttgaag gaagtccaag tatccaattt taaggatgcc    180

tattagagca gttataagag agtgtctctc tttctctctc ttctttcttt ctcttggtag    240

gagtatgcag gaggtcattt aaaagccaga tagtgataca aatcacaatg cagaaaaaca    300

tcccgtgga ctcctccctg tcctatgttt gacattctta aaatctatgt cccaggtctt    360

gaaatcttta ataatctac catgttcttt ggcctgccct gggaaatcta tttcagtacc    420

agagctatgc tggttacaca ccttttctga ctcatgttcc caagtgattt tattccagat    480

acgatttggg gacagttacg tgtactgttc tgatatcttc ctaaaaggaa attattttgg    540

aagtaaagtc actgataaaa tcaactcagg aaaatgcact ttgtaaatat taaaatataa    600

acattattaa aggccatgct gtaaaatact aattgatttt cctgtgtagc agttacaata    660

gaacacgata gatctctang gggagagtga aaggact                             697


<210>    56
<211>    617
```

<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(617)
<223> n is a, g, c, or t

<400> 56
tggattgcga gcggataaca atttcacaca gaattcattc aatgaactgt tatggggtct   60

cacattgtac caggcactgg ggattcagct tccagttcat agtctgcatg caaaccgaca   120

tgcaggtaga catgcagaca gaaaatcgga acgcaacacg gtaagtgcta tgctagagaa   180

tgagaaggac tgtcagtaat cacaaccacc tttcactggg ttccttcagt gtgccaggct   240

cgtgtacatt attttgttta gtgctcacaa ttgtatggac tgtgtactat catttgccag   300

attatatgga tgaagaaact agactgaggg ggttaaataa ctcgtccaag atcatgcaga   360

caaaaaacca cagagattat tttccaatac aaactctctg gctgtacagc tcaagttctt   420

aaacactggg ccaaccagtc tgaatctgag aggaggcatt ctaaggctta caggtaagtg   480

ggaattgaaa gggttgaggg aagccttctg gaggagatgc cattacactg aatgttgaat   540

gagtaggagt tagctatctc cagaggggta gtggctgtga aggggcgagg ggtagagggt   600

ggnaagggga tgaattg   617

<210> 57
<211> 803
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(803)
<223> n is a, g, c, or t

<400> 57
cctgcagcta gcttgccaaa cctacaggtg gggtctttca agatctgctg acagtgaagc   60

taaatctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc   120

tcttaaacaa tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa   180

ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc   240

ttggtaggag tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag   300

aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc   360

aggtcttgaa atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt   420

cagtaccaga gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat   480

```
tccagatacg atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt        540

attttggaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa        600

aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgtgtagcag        660

ttacaataga acaacgatag atctctaagg ggagagtgaa aggacctcaa tttgagaaac        720

gtgaggcagg aaaagtttca aatattatat tcaagagtgt acctaagttg ttacttaaag        780

acaattctnc acttaaataa acc                                                803
```

```
<210>  58
<211>  786
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
<222>  (1)..(786)
<223>  n is a, g, c, or t

<400>  58
gngnggnaat gtgcagncgg ntaacaattt cacacagnaa ttccatttcc ctcaacaagc         60

aggagaaatt ttctcaagag tttaccagaa gtcactctta acgtcaggct tgcaaatttt        120

aaaaagcatg aaaaagaacg tctactacat aatcctccag gcacattcca acacgctgcc        180

aacagtattc ctgaaaatcc tctgtcaaac ccctccataa atcatagcct cagagctctg        240

tgtgtgtggc tgcagcaggc tcgtagctgc agagcacttg catggaggag acatgcgctc        300

aggaactgca ccgccgcatt ccgcagaagc cacgcgactt acttccctct gctgcatgtt        360

aacctgtgct atgttctaga tcttactta gttagtaatt caacaacagg agtcatgtgg        420

gctggcaagt agtcagctga aaactaacat gtgaacagaa ctctcagggg caggcctcca        480

gcaagctccc acccgagtca gtactgctcc cgccttccct tcagcttgtg ggtgggtact       540


accttctgaa gcctcacaaa accccccatct gaaagaagag gaaactgaga cacggtgaga       660

catggtgccc ctcgcccaaa gtctgacagt ttgatatggt agagccagga atccatccca       720

gggnagtggg ccagaaggta gtggctgact gccatgcccg aggacgtccc caggagctgc       780

cgtgaa                                                                   786
```

```
<210>  59
<211>  837
<212>  DNA
<213>  Canis familiaris


<220>
<221>  misc_feature
```

<222>   (1)..(837)
<223>   n is a, g, c, or t

<400>   59
tctggnnccc cgggacgtnn ttgggagctg ccctgagctc ccacctgctg ctgccagtac   60

tagcacaggg tcctcaagtg atggctgctg gtgaattatt tagaatctcc atgggcaggg   120

cattctgctt tttagcactg tgtcttgacc tgttccaaga ccatcttcca aggagagcca   180

gcagctggtg ttgtaagttc ttcccatgac aaataagccc aagacctcac ttaggaaaca   240

tacaatgatt atatgatctt gggagtcagc cctagaaggg cccttcttct cttgcttcaa   300

gctaaaaaga ctctggacaa caaaagaggc agtggctgct aagtaacttg caactaccac   360

ttcagtctca ctgcagctgc aaagatagga acagagaagt tttaggtgag aaactccttt   420

ttcccaagaa actgtgatga accagtgtta cagtttaggg agagagctct gtagacaagg   480

agggacctaa ggaccccag   gactcaccac ccccacacct agctccctg   gtcacctggt   540

acgtaagcag gtaggctctg cttagcatag tgctaagatc acatcttgct cagagtgtac   600

aaactcagga aagctggcat taggtagtat cacaagtgaa aaaatacctc aaccagtggc   660

cattggaagt gcggaagtac atgccatact cactgcaagg ttctccattc cagctgccgt   720

actgtgtaat acgacttaat atcttcagag natcaaggtt aatttcaaat ttgtgtcttc   780

aaagaacatt tcttttttnnt tcttttgggg ncagtactgc gcacatttta actagga   837

<211>   866
<212>   DNA
<213>   Canis familiaris

<220>
<221>   misc_feature
<222>   (1)..(866)
<223>   n is a, g, c, or t

<400>   60
ttgtcgagcg gataacaatt tcacacagna attccagcac catgcactct ctgagacagg   60

tgaggatttt gcagcagctg ataaggacac aagtgaacag gagcataata atgaaaacac   120

aaagactagt tagctgttac tacttgcttc tagggcttct agtgttctct gttgtgatac   180

ttggtcaaat gttgtttggg agtcactgaa gaatgcttca tcatttgcaa agataggacc   240

ctaacttgta agccccttaa attaaaagaa tgctttttag tacaaaatta atgatcttag   300

tcacaaaaag caaagaagaa atcaaaatca caaagtcatc attcaaagtt gtattcttta   360

tagcaaaaat ggggcaagct acaggattgc caaaagtctt ataaaacagg aggaaggttt   420

atgaaatgat gctcagagag aatgcagaat gtgctattag cacaaatcct ttctgaaatg   480

gaacctgagc aaagtgatgg catttgatgt agaggaatag ccaccatcac atatgtgtga   540

gagaaaatag tttgctttgg ggatgaacaa taccaccgtt gtacaaagca tgaataagca   600

cttggaaaat gtatagtatg tataacagag ggacttttat ctgtttggca ttgaaaatca   660

atgccattaa aagtaggaac aattggttat tgggnctgat tttttaaaag aattcattta   720

tttnttttng gggganagaa nnccccccc cctntnaccc cnggggaaan annnaggggn   780

aaaaaanaat ntnnagccna ctntttttctt nntgggnccc cgggngggggg ctttancnca   840

aancccngna aannannntn ngnccn   866

<210> 61
<211> 886
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(886)
<223> n is a, g, c, or t

<400> 61
ttgngaaccc gcttgccaaa cctacaggtg gggcctttca agaacataag cccaaataag   60

cactggcaca tagtaggagc agcataaacg ctccccctcc tattcctaac ccaccaagaa   120

ttctagattg acagtttttt ctttgagtat tttaaagatg ctgcttccct gacttcttgt   180

ttgcaaattt ctgatgagaa atctgctgtc attttatctt ccttcctttg cataatgatg   240

tatctttttc tctctgcttt taagattttc attttatcac tggttctaag caatttaatt   300

atgatgttcc ttggtatagt gctcttcata tttctattag gagtttgttg agcttcttgg   360

atttgtgagt ttatagtttt tatcaaattt ggcaagtttt cagctactat ttcttcaact   420

ttttttttcc tgtcctccct tgactcctcc tcattcccat atttctcctg tccttcaggg   480

actccagtta tctgtatgtt aagctcattg ataccctatt tgtgtatatt ttaaggcttt   540

ttattccctg tatttcattt tggatagttt ctactgcaat gttttcaggt tctttaacct   600

cttttttttt ttcccccccag taatgtctaa tctgctcttc atcccaaaga catgtagtgg   660

tgtgtgtgct aaaaatccca gacaatgttt ttatgattcc taggtatttg ctttggggct   720

tttcaaagat tttccatatt tctacttcct tggccatata gaatgcggnt attattattt   780

tttagnggcc tatgctacta aatcctataa ttnctgggac tccnttgatt nagnntnncc   840

tttttattta ttnattaagn anggttttat tgggagttng attncc   886

<210> 62
<211> 728
<212> DNA
<213> Canis familiaris

                                    43

<220>
<221> misc_feature
<222> (1)..(728)
<223> n is a, g, c, or t

<400> 62
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ggattgtcag cggataacaa tttcacacag aattcccagg acccagcatg atgcctggtg       60

tgcacatggg tgggccctcc tatgtaagcg tcaccactcg ggagcagtgg cggggatgcc      120

tggatgcgcc ggctcctgcg tgtagggtgc tatcaggaca ttgctgggtt gccacctctg      180

tctgaggctc cagagagcga ggggacaccc cacatcatga atgccctgtg gggttaccag      240

tgggggcaat tacctgcatt gctcctgggc ctcagcggcc tcatctgtga aatgggtaca      300

ttcatatcac gtatgggaga gggctgccgt ggggtttaat ggaggcaacc catttgagcg      360

ctgggcccgg caccgctcct gctcttactg tgactatggc cagcgtcact gttgcagggc      420

cttgaccggc cggggtggac gctggtgcca ccgttgctct ctcccagggt gggaggagac      480

aggcctgcgg ggcggactca ccgtggcgtt gacggtgagc tggtaggcct gcgtggtctc      540

gtagtccagc tcgcggacca ccgtgacgat gccgcgggcg ctgtcgatgg cgaacaacgg      600

ggaccggggc tggaaggagt acaggacgct gcccctgca ccaagtcggg gtccgtggcg       660

ttacgataaa atgggtgtcc ccaccggcgt gttctggggg ccaagcaaac aaccaaggtg      720

agtgggct                                                               728
```

<210> 63
<211> 785
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1)..(785)
<223> n is a, g, c, or t

<400> 63
```
attgtcgagc ggataacaat ttcacacaga attcctaaaa cccttactgt tgtttttata       60

tggcacttcc tgatgtgatt gcaggctttt agcaaagcca tttttgttaa caaaaaatga      120

tttaaattct tttaaacaag tgtttagtga caagtcagta tttagtcatc tagttattga      180

tacagcaccc ataaaattta tcactgaggg gagggatcag gaggaaatgt gggcattcta      240

acttaatgat taataatatg tgtctataac aaatgtgatg gctaagttat aaaatatta       300

aaaaatttt tcttgcaggt atttataaca gcaatgatgt agcagtatca tttccaaatg       360

tggtatctgg ctcaggatct agcactcctg tctccagttc tcatttacct cagcagtctt      420

ctgggcattt gcaacaagtg ggagcactct ccccatcagc agcatcatct gcaacccctg      480
```

```
ctgttgctac aactcaggta atcattacag tgctatgaag taacctgtag atggctttgt      540

cgttttgaa agtgagtttg attggagaag aaagaaacct tgtatagaaa ccttcctata       600

taaattccta taggaattta taagtatctc catttgtttt gacacgttag tggatataat     660

agacatttt atgtgatatt catgagaaag gacaaaagaa tacattggca ttaactgatt        720

ctttcagtt tctgagtttc taatttttcc tgaagatgna aacaaaaatt tggggggaac       780

tttta                                                                 785
```

```
<210>    64
<211>    981
<212>    DNA
<213>    Cercopithecus aethiops


<220>
<221>    misc_feature
<222>    (1)..(981)
<223>    n is a, g, c, or t

<400>    64
```

```
ttggnaancg tcagaccaag tttactcata tcggatccaa agtgcttgag actgcatttt      60

tttcaaattt tgcaatattt gcattataat caccagttaa gcatccgtaa tccaaaaatc      120

ctaaacctac aatgctctaa taaatatttc ctttggctgt gttggtgcaa aaaatgtttt      180

ggattttgga agacttcaaa tttcacatta gggataccct gagtggaaaa aatagttttt      240

gtttttaaga ttctttcact caacaacaat caacaaggta gacttctgtg atcaaatgtg      300

tgaggatttc tccccaccaa taagcaatca attctgcagc agacaccaag tgggtatcct      360

ccaattcaag tctgacatta cctacctgga gaaagcgtca gatctcacag gttgatggct       420

cagtcccaca agactgctcc ctacttctga tgtcaatcac aagccacagt ttgttttacc     480

tgtgcttcta actgactgga tataaactgg gaatctcatg agcccctctt tgggttcggt      540

taatttgcta gagtggctca cagaactcag ggaatcacat ttattagttt attataaagg      600

atatacagtt gaagagatac acatggcaag gtatgccctc cctgggaaca ccactctcca     660

ggaacctnct tttgttcctg tccagaagct cttcgaatcc tctcctcttg ggccttttat       720

ggagacttna ttagatgggc atgactgaca cacatgtaga aatgtgactg gagaaaaaat     780

atatgatcta atattaatag actggggaaa ctcancaggg cctgtntgtt caaattnttc      840

nggncntttt gggtagcatt ncttnctcca gggttngggg gngnacnttt ttgaaagaaa      900

gtntttgacc ctanncaaaa gnggggggaag annaantnct ctttnggcag nnaaaaaaaa     960

aaaaattttt ttttnggnt n                                                981
```

<210> 65
<211> 981
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(981)
<223> n is a, g, c, or t

<400> 65

```
ttggnaancg tcagaccaag tttactcata tcggatccaa agtgcttgag actgcatttt        60

tttcaaattt tgcaatattt gcattataat caccagttaa gcatccgtaa tccaaaaatc       120

ctaaacctac aatgctctaa taaatatttc ctttggctgt gttggtgcaa aaaatgtttt       180

ggattttgga agacttcaaa tttcacatta gggataccct gagtggaaaa aatagttttt       240

gtttttaaga ttctttcact caacaacaat caacaaggta gacttctgtg atcaaatgtg       300

tgaggatttc tcccaccaa taagcaatca attctgcagc agacaccaag tgggtatcct        360

ccaattcaag tctgacatta cctacctgga gaaagcgtca gatctcacag gttgatggct       420

cagtcccaca agactgctcc ctacttctga tgtcaatcac aagccacagt ttgttttacc       480

tgtgcttcta actgactgga tataaactgg gaatctcatg agcccctctt tgggttcggt       540

taatttgcta gagtggctca cagaactcag ggaatcacat ttattagttt attataaagg       600

atatacagtt gaagagatac acatggcaag gtatgccctc cctgggaaca ccactctcca       660

ggaacctnct tttgttcctg tccagaagct cttcgaatcc tctcctcttg ggcctttat        720

ggagacttna ttagatgggc atgactgaca cacatgtaga aatgtgactg gagaaaaaat       780

atatgatcta atattaatag actggggaaa ctcancaggg cctgtntgtt caaattnttc       840

nggncntttt gggtagcatt ncttnctcca gggttngggg gngnacnttt ttgaaagaaa       900

gtntttgacc ctanncaaaa gnggggggaag annaantnct ctttnggcag nnaaaaaaaa      960

aaaaattttt tttttnggnt n                                                 981
```

<210> 66
<211> 1005
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(1005)
<223> n is a, g, c, or t

<400> 66

```
ctnagctngc ttgccaaacc tacaggtggg gtctttcaaa aaacagacat gcagacttta        60
```

```
acagataata aggttttga ggttttccgt ttatgtattt actcgagaaa gcaagagctt      120

tatttattta ttttgagac ggagtttcgc tctgtcgccc gggctggagt gcaatggctc      180

catctcgtct cactgaaacc tctgcctccc gggttcaagc gattctccca tctcaacctc      240

ccgagtagct gggattacag gcgcgcgacg ccacgcctgt ataaaatac taaaaatgca      300

aaaataattt ttgtattttt agtagagatg gcgtttcatc atgttggcga aactccaggc      360

tggtctcgaa ccctgacctc ggtgatctgc ccgcctcggc ctcccaaagt gctgggatta      420

caggcgtgag ccaccgcgac cggccaagag ctttataaag atggaaaacg aagcagactt      480

tctgcccaag ccatgctttt ggataaggat tacactactt tgaaatctta catatatagc      540

acttggccaa ctatcaaaac tgcacaaacc ttcactaatt gcaattattc cctttaacat      600

ctcgagttac cccaatccgc acaaaacaag tttagtgccc accaggtaat aatacattca      660

ggaaaataat tccaagaaca gacgtttaag aactacagag aaaaacatac ttttttctac      720

aagaaaaaat cttagaggac agtaccaggg nccttatctc tgttagcatg atttatattt      780

cacgtaacgt tggcccagtc actgctncat tntaaancna tagccanggc anatagaaag      840

tctgaacana ttgacngcna ngggtttaaa ttttttacca ggnaacaaan cctggcaaac      900

tgccancang ggtgcccaaa tgctggnctn gggtccctgg aagnaaacgg agggctttga      960

attttttcc ntttnggaac ngncnnggnt ttnggcnaan tnttc                     1005
```

```
<210>  67
<211>  863
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(863)
<223>  n is a, g, c, or t

<400>  67
nttttgggng nntancttnt ananatnngc caattattgg ggggnacctt catcataagt      60

attaatataa taataataat aagtaatagt aactagtaac aacaataaaa aggaaatcag     120

cggaaagtca ggaaaaatgt taaaaaaaaa ttggaataac ttactgtagc tgaagatcaa     180

aaaaatctca ctgtaaaaaa acaaaaataa aaatagccca gattagaaaa acgggaggtg     240

caaaaatgtc aagtcagtaa agttcatttc ttttctcttt ccaaaagcag tttccacaaa     300

aaccgcaagg ataaagtttt cagtagcaga caagcaaagc cctttcgaca tcatcaatca     360

atcttaaaaa tacacgagga agtagagagg tcagtttatg agaggctaaa aggctcctcc     420

tcctctaacc caactgctgc agaaaaaata gaaatagaaa ttttaaaaat tacatcttaa     480
```

47

```
atccaggtcc cggttttgga aacaattaaa aaaaaaacac ctgtacattt gccgtagtgc        540

acaccaagtt gcatcattat gtttaaaatg tctttataaa atcagttttg gaatggaatg        600

tgtgtgttct ggaagggtgg ggaagggagg ttaaaaatca aagctgagct ccagtgagta        660

gggatggggt tcgccttgct gccctgtgaa agggaaagga cagatnagtc aanttnctaa        720

aaatgtntgc cctaancccn anaaaaaact ttgnnttttng aantaaaaat ttggtaagct        780

ttaaattccc tgggngggaa nccncntaaa naccttтnca ngnnngntta aaattttaan        840

aaaangggnn naaaaaaaaa ncc                                              863
```

```
<210>  68
<211>  918
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(918)
<223>  n is a, g, c, or t

<400>  68
cnnttctgg nngatnaaan tnnttnnnna nttcnccaat nnattggggg gaannnttca         60

tcataagtat tnatataata ataataataa gtaatagtaa ctagtaacaa caataaaaag        120

gaaatcagcg gaaagtcagg aaaaatgtta aaaaaaaatt ggaataactt actgtagctg        180

aagatcaaaa aaatctcact gtaaaaaaac aaaaataaaa atagcccaga ttagaaaaac        240

gggaggtgca aaaatgtcaa gtcagtaaag ttcatttctt ttctctttcc aaaagcagtt        300

tccacaaaaa ccgcaaggat aaagttttca gtagcagaca agcaaagccc tttcgacatc        360

atcaatcaat cttaaaaata cacgaggaag tagagaggtc agtttatgag aggctaaaag        420

gctcctcctc ctctaaccca actgctgcag aaaaaataga aatagaaatt ttaaaaatta        480

catcttaaat ccaggtcccg gttttggaaa caattaaaaa aaaaacacct gtacatttgc        540

cgtagtgcac accaagttgc atcattatgt ttaaaatgtc tttataaaat cagttttgga        600

atggaatgtg tgtgttctgg aagggtgggg aagggaggtt aaaaatcaaa gctgagctcc        660

agtgagtagg gatggggttc gccttgctgc cctgtgaaag gagaagggac agattgagtc        720

agagttcctc aaaaatgttg tgccctaaac ccccaagaca gaaacatctt gtttattntn        780

gctaacacaa tntttntgna naatnatnaa cctccccngg ggagggnacn ccctnnnnaa        840

aannncccтt nccanggant gnnttnaaan tttttnaana tnantggggg nanaaaatna        900

acnaanccct gnnaattn                                                     918
```

```
<210>  69
```

```
<211>   887
<212>   DNA


<220>
<221>   misc_feature
<222>   (1)..(887)
<223>   n is a, g, c, or t

<400>   69
tncantcttt nnnnggcnna nacgcgcgnc nantcgccaa tnactggggg ggnancttca      60

tcataagtat taatataata ataataataa gtaatagtaa ctagtaacaa caataaaaag     120

gaaatcagcg gaaagtcagg aaaaatgtta aaaaaaaatt ggaataactt actgtagctg     180

aagatcaaaa aaatctcact gtaaaaaaac aaaaataaaa atagcccaga ttagaaaaac     240

gggaggtgca aaaatgtcaa gtcagtaaag ttcatttctt ttctctttcc aaaagcagtt     300

tccacaaaaa ccgcaaggat aaagttttca gtagcagaca agcaaagccc tttcgacatc     360

atcaatcaat cttaaaaata cacgaggaag tagagaggtc agtttatgag aggctaaaag     420

gctcctcctc ctctaaccca actgctgcag aaaaaataga aatagaaatt ttaaaaatta     480

catcttaaat ccaggtcccg gttttggaaa caattaaaaa aaaaacacct gtacatttgc     540

cgtagtgcac accaagttgc atcattatgt ttaaaatgtc tttataaaat cagtttggga     600

atggaatgtg tgtgttctgg aagggtgggg aagggaggtt aaaaatcaaa gctgagctcc     660

agtgagtagg gatggggttc gccttgctgc cctgtgaaag gagaagggac agattgagtc     720

agagttcctc agaaatgttg tgccctaacc cccaagacag aaacatctgt ctttgcagct     780

aacacatttt ggnaagcatn acatncactg ggatggacag ccncntaaaa aaccttnncn     840

ngncnnnttt naantttaa nnnaaagggg nnnaaataan naacccn                    887


<210>   70
<211>   897
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(897)
<223>   n is a, g, c, or t

<400>   70
ctttggggng tnnttcanac ntttancac nntnntcgcc antccncttg aggggnaaac       60

ccatcgcctt ctatcgnctt cttgacgagt tcttctgagc gggactctgg ggttcgaaat     120

gagctagccc ttaagtaacg ccattttgca aggcatggaa aaatacataa ctgagaatag     180

aaaagttcag atcgaggtca ggaacagatg gaacagggtc gaccggtcga ccggtcgacc     240
```

49

```
ctagagaacc atcagatgtt tccagggtgc cccaaggacc tgaaatgacc ctgtgcctta          300

tttgaactaa ccaatcagtt cgcttctcgc ttctgttcgc gcgcttctgc tccccgagct          360

caataaaaga gcccacaacc cctcactcgg ggcgccagtc ctccgattga ctgagtcgcc          420

cgggtacccg tgtatccaat aaaccctctt gcagttgcat ccgacttgtg gtctcgctgt          480

tccttgggag ggtctcctct gagtgattga ctaccgtca gcggggtct ttcaatgatg          540

gtgatgatga tgatgataat gacactgatg atttttaacc ggattaaaat cgagttttc          600

tgaatgtttc taagaatttc tccggcctcc tgattgactt tggagttttg catcttggga          660

gagaaagcga aggcattagt attttaagt ggattgatca cataaacctt ttctctccca          720

accccaccct tgcccttatc cccttcccca cactgaacag aattttactg gctgntaagt          780

ctatgacctt attttttcct gatctttaac ttaactgntt tagagcatct ntggacgncn         i840

ggattttnaa attttttnat tttnggnttt ttnntttnaa annttnnatt gggaaan           897
```

```
<210>   71
<211>   878
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(878)
<223>   n is a, g, c, or t

<400>   71
tcggggngnn ctccactnnt gntgcnnntc nncgccantc cncttgnggg gnaaaccatc          60

gccttctatc gncttcttga cgagttcttc tgagcgggac tctggggttc gaaatgagct          120

agcccttaag taacgccatt ttgcaaggca tggaaaaata cataactgag aatagaaaag          180

ttcagatcga ggtcaggaac agatggaaca gggtcgaccg gtcgaccggt cgaccctaga          240

gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg ccttatttga          300

actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct tctgctcccc gagctcaata          360

aaagagccca caacccctca ctcggggcgc cagtcctccg attgactgag tcgcccgggt          420

acccgtgtat ccaataaacc ctcttgcagt tgcatccgac ttgtggtctc gctgttcctt          480

gggagggtct cctctgagtg attgactacc cgtcagcggg ggtctttcaa tgatggtgat          540

gatgatgatg ataatgacac tgatgatttt taaccggatt aaaatcgagt ttttctgaat          600

gtttctaaga atttctccgg cctcctgatt gactttggag ttttgcatct tgggagagaa          660

agcgaaggca ttagtatttt taagtggatt gatcacataa accttttctt tnccaacccc          720

acccttgccc ttatcccctt ccccacactg aacagaattt tactggctgn taagtctatg          780
```

accttatttt tcctgatctt taactnactg ntttagannt ctctggacgn cggnntttna   840

aatttnttat tttgggtttt tantttaaan cttnattn   878

<210> 72
<211> 964
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(964)
<223> n is a, g, c, or t

<400> 72
cttctgggnn gannnaanca nttcgnncan nnctccncca atctacttgn ggggcaaacc   60

catcgccttc tatcgttctt cttgacgagt tcttctgagc gggactctgg ggttcgaaat   120

gagctagccc ttaagtaacg ccattttgca aggcatggaa aaatacataa ctgagaatag   180

aaaagttcag atcgaggtca ggaacagatg gaacagggtc gaccggtcga ccggtcgacc   240

ctagagaacc atcagatgtt tccagggtgc cccaaggacc tgaaatgacc ctgtgcctta   300

tttgaactaa ccaatcagtt cgcttctcgc ttctgttcgc gcgcttctgc tccccgagct   360

caataaaaga gcccacaacc cctcactcgg ggcgccagtc ctccgattga ctgagtcgcc   420

cgggtacccg tgtatccaat aaaccctctt gcagttgcat ccgacttgtg gtctcgctgt   480

tccttgggag ggtctcctct gagtgattga ctacccgtca gcggggggtct ttcaatgatg   540

gtgatgatga tgatgataat gacactgatg atttttaacc ggattaaaat cgagttttc   600

tgaatgtttc taagaatttc tccggcctcc tgattgactt tggagttttg catcttggga   660

gagaaagcga aggcattagt attttaagt ggattgatca cataaacctt tttttttncca   720

accccaccct tgnccttatn cccttnccca cactgaacag aaanttactg gctggnannn   780

natganccta nttttncngn ncttnaanta acnggnnnna anaaancnng gcnnccggnn   840

nnnaaaaaan ttnnnnnnng nngntttttt naaaaancnt nnttnnaaaa ntaaaancgg   900

nnnnnaaaaa nggggggggn cnncnnancn tnannnnggg ngggttttcc nnnaancntt   960

ttcc   964

<210> 73
<211> 986
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(986)

<223> n is a, g, c, or t

<400> 73
catcnttctg nnnngnaana aacgtncnnn nnncnnctcc cnaatttaac ttgggggggn   60

aaaancatcg ccttctattt ttcttcttga cgagttcttc tgagcgggac tctggggttc   120

gaaatgagct agcccttaag taacgccatt ttgcaaggca tggaaaaata cataactgag   180

aatagaaaag ttcagatcga ggtcaggaac agatggaaca gggtcgaccg gtcgaccggt   240

cgaccctaga gaaccatcag atgtttccag ggtgccccaa ggacctgaaa tgaccctgtg   300

ccttatttga actaaccaat cagttcgctt ctcgcttctg ttcgcgcgct tctgctcccc   360

gagctcaata aaagagccca caacccctca ctcggggcgc cagtcctccg attgactgag   420

tcgcccgggt acccgtgtat ccaataaacc ctcttgcagt tgcatccgac ttgtggtctc   480

gctgttcctt gggagggtct cctctgagtg attgactacc cgtcagcggg ggtctttcaa   540

tgatggtgat gatgatgatg ataatgacac tgatgatttt taaccggatt aaaatcgagt   600

ttttctgaat gtttctaaga atttctccgg cctcctgatt gactttggag ttttgcatct   660

tgggagagaa agcgaaggca ttagtatttt taagtggatt gatcacataa acctttctc   720

tcccaacccc acccttgccc ttatcccctt ccccacactg aacagaattt tactggctgt   780

taagtctatg accttatttt tcctgatctt taacttaact gntttanagc atctntggac   840

gnnngnattt naaanntttt tatttnggnt tttnatttta aannttnatt ngnaaanntt   900

naactgggct gnanaaaagg gnggggncta ctnaaantnn nnacgggagg gntttncctg   960

nanncanttn ctccnnttcc ntgaan   986

<210> 74
<211> 748
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(748)
<223> n is a, g, c, or t

<400> 74
ttttttgcnt taccgtatcg ccgctnncga ttcgcagcgc atcgccttct atcgccttct   60

tgacgagttc ttctgagcgg gactctgggg ttcgaaatga gctagccctt aagtaacgcc   120

attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg   180

aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaaccat cagatgtttc   240

cagggtgccc caaggacctg aaatgaccct gtgccttatt tgaactaacc aatcagttcg   300

cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc   360

```
accctcttgc agttgcatcc gacttgtggt ctcgctgttc cttgggaggg tctcctctga      480

gtgattgact acccgtcagc gggggtcttt caatgatggt gatgatgatg atgataatga      540

cactgatgat ttttaaccgg attaaaatcg agtttttctg aatgtttcta agaatttctc      600

cggcctcctg attgactttg gagttttgca tcttgggaga gaaagcgaag gcattagtat      660

ttttaagtgg attgatcaca taaaccnttt tntcttccaa ccccaccctt gcccttatnc      720

ccttncccac actgaacaga attttact                                        748
```

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<210>  75
<211>  881
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(881)
<223>  n is a, g, c, or t

<400>  75
tnctttgcgg acccgtatcg ccgcttccga ttcgcagcgc atcgccttct atcgccttct       60

attttgcaag gcatggaaaa atacataact gagaatagaa aagttcagat cgaggtcagg      180

aacagatgga acagggtcga ccggtcgacc ggtcgaccct agagaaccat cagatgtttc      240

cagggtgccc caaggacctg aaatgaccct gtgccttatt tgaactaacc aatcagttcg      300

cttctcgctt ctgttcgcgc gcttctgctc cccgagctca ataaaagagc ccacaacccc      360

tcactcgggg cgccagtcct ccgattgact gagtcgcccg ggtacccgtg tatccaataa      420

accctcttgc agttgcatcc gacttgtggt ctcgctgttc cttgggaggg tctcctctga      480

gtgattgact acccgtcagc gggggtcttt caatgatggt gatgatgatg atgataatga      540

cactgatgat ttttaaccgg attaaaatcg agtttttctg aatgtttcta agaatttctc      600

cggcctcctg attgactttg gagttttgca tcttgggaga gaaagcgaan gccttantat      660

tttttagngg gtnggnnaca tataaccttt ttttttccaa ncccccccctt nccctttttnc      720

cctttccccc actgaaaaaa attttacngg ctgnnaannn tnnnaccntn ttttnccnnn      780

ncttnannna annggttnaa gaccnnnnng ggccnnnggn tttnaaantt ttttnttnng      840

ggnttttnnt tnnaancnnn cnttggnaaa ntttnaanng g                         881
```

```
<210>  76
<211>  906
<212>  DNA
<213>  Cercopithecus aethiops
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```
<220>
<221>  misc_feature
<222>  (1)..(906)
<223>  n is a, g, c, or t

<400>  76
cannnttctg gggngtnnnn aactnannnn nnnnatcgcn nccacantnn nnttggggg      60

aaaaacctga atacatttgt ngttatttcc cttagatctt tttttttttt ttttttttt     120

ttgagacatc tcactctgtc acccaggcta gagtgaagtg gcacaatctc tggctcactg     180

caacccccac ctgcctggtt caagcgattc tcctgcctca gcttcccgag tagctggtac     240

tataggtgtg caccaccaca cctggctaat tttttaaaa aatatttta gtggagatgg      300

ggtttcacca tgttgaccag gctggtctca aactcctgac ctcaaaggat ccacctgcct     360

tggcctccca aagtgctggg attataagca tgagccacca tgccagcctg tttctttag      420

atcttgattt gatattctgg atatgaatga aagaaaatta atgagtgttt caaagtctaa     480

ataaggaagc tccacagata atattaacat ttctctgatc tagtcatatt tattattgtg     540

tttcaattag aagtggctgt aggctctgaa agacacacta taaataaagc ctcccctca      600

tacaccctca ctcacaccca cacttacacc aatgcaattt ttagacagaa acacaagcaa     660

gaaataggat agattttttt taaaaaatgg gcattggtta aattttctgg tcatattaaa     720

aaanntnttt nagaactccc aanggggggc cattaataga gacctnattc nctgnnggaa     780

nnaaannggn aaattncnan aattnctnac aatntttagg ganttgangn aaaatnttnn     840

gtnnntgnna ctttcctagn ggncnnnttn ngccctatnc ccaggnnttt tatnctaaac     900

cccntc                                                              906
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```
<210>  77
<211>  909
<212>  DNA
<213>  Cercopithecus aethiops
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<220>
<221>  misc_feature
<222>  (1)..(909)
<223>  n is a, g, c, or t

<400>  77
cntcttnngg gngttnaanc tgncntnnaa tgcntcacat tnattnnggg gaaaaccgta     60

ctgacttatt atgagaggtt tctgctcttg ttaggatcca gtaggtttga ggtgcaacta     120

ttcctctact ttactcttcc acctcccaga gaactctgcc aagaaccatg ttaagactgc     180

tttctgcttt aactactaat agtcttgatt ataggaacgg aatttgtgta tcaagtaggt     240
```

```
tctaagaact taacataaaa actggctatt aatgcatttg caaaatttgc attttaaatc      300

caaggcaaga acaggtcagg caaaaatgga atccaaacac caaattgtta aaagttttaa      360

gtccatttct cttgttagtt tgcaacttaa attactaatt ctctaatgtt ttagagcaga      420

agttggtaaa ttgtttctgt aaaaaaattg tttctttaaa ttgtttcata atcaaaattt      480

taggttgtgt aggtgatact gtttctgttg aaattattta atctaaataa atggacatag      540

ctgtgttcta acaaaacttt atgattaacc tgacaggcca gatttgaaat gttagcaggt      600

ttgcacaccc ctactttaga aaaactcagt ctttatagct tccagttaca agatgtatct      660

ttttttttt tttttttaaa taagacagta ttattncaaa tgtcgggtgg ctcataccna      720

aatttgtttc cccnttcttn anttttcnaa angtggggcc caaanacttn aaaaggtngn      780

anncntttnn nntaanaaaa nanccattta ggggnttntn caacccctnn aaaaantttt      840

tttcttnaaa aanaantnca naaaannntn ctnaaaaaan naaagggggcc cacccnttnt      900

ttttaaaac                                                           909
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<210>  78
<211>  890
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(890)
<223>  n is a, g, c, or t

<400>  78
gnnntncnnc tttnnnngat cagccgcncc ncagnncccc accaatccna cttggtgtaa      60

acccccccagc agggtcttgg gctttctttc tgcttctcca aaatgggcct ggcttccag      120

gagacagccg agagcgcctc gcccctgctg gaagggcagc ctgggagctg gagttggcaa      180

acgggagggg acgggaggag gcccagggga ggggcgtct tcccttagct ttcagcgaca      240

tctgctggcc gtgcgctgaa ctgccgctac cccagaggcc agctggagac caattttgag      300

ttgtgagcag ggaaagagag gaggggttcc aggacaatca ggtctggagc ttccagaaac      360

attccaaaaa cacagtttag gcttttaat tgttcactca gtcattctcc cggggtctag      420

ggagaaatcg gactcagact cggatctttg gggacctacc gcagcatgat aacccaggtg      480

tacctggggc tcatgggggc ctgggatca gggaggcccc tcacctgcat tcactgtgtg      540

ccaagcactg gcctacatca ctgacatttg ctgtctcgct gcgggtgctg tgatcttgct      600

gctgtgctca tttgacagat gaaaacgctc aggttgtgag agaaccccaa agccagagga      660

ttcccttgat cactcccctt cgttcatgcc catagtcaat ccttcttcaa agcctatccg      720
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```
tcccacctcc aaagcacacc atggatgccc atccttggcc catcatcgtt accctctnag      780

tgccagcctg cctgancccc tcanttnaag tcccgctccc tggccttttg cagaagcatc      840

ccaccagaat ctncaagcca cccctcccna ntttnttntt cccaaatggc                 890
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```
<210>   79
<211>   965
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(965)
<223>   n is a, g, c, or t

<400>   79
ntttctggnn gtnacagang gggngccnnn cccccccatn aactgggggn aaacncncc       60

agccccaagg tggccattgt cagggaggtg cttgctatgc agatgtgccg ttcaaaggca      120

tgcagatatg aaagcatcgc tccctcaggt gggagacaat gggaaggtcg agagcactgt      180

ggttaggagc aaggctttgg aattagcagt ccctgcattc aaatcctagc tttacttgcc      240

tcatgacagc cgtctgtcct tgagcaaaat tgtttaacct ctctggacct gtctatatct      300

gtaaaaaggg ccaacatggt gtacccaaaa gccttgtcgt ggtgatctca ttaagatatt      360

tcatgtgaat atgtgctgag tggcctcacg taggaggtgc ttactgactt ctcccaagcc      420

ccctcctctt catcgctact gcccgtctgc gtatcctcca gcctcctccc acgctttctc      480

tcactgcact ttttgggggt gagggaggcc atttctgagt cacttgctcc tggacttgat      540

gaattccatt cgtgtggcgg gggcagcagg gcccagtgtg aaccagcagc tccccaaccc      600

tgcccactat accactcaag tgagtccaag ctgtgatgcc cctggctgcc tcccccactt      660

cccttgagcg agctgggagg acaaagattg gactctgagg atcagcctga gacttaagat      720

ggaggctgtg ttcccgagag cccagggtgg gcatgccagg aagcactctg gctccacgga      780

atgctgcact gccccggggc tggcanacca ncacttcctt gtnttnctgg gtctnacagn      840

cncancctgg cctgggctgt ttttgcntgn tgnacctgcc tnaaannggn aaancctggn      900

ancctggagn cttccnaggt ttngnttttc caancncnca aaattangnc naaccngnct      960

nnggc                                                                 965
```

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<210>   80
<211>   891
<212>   DNA
<213>   Cercopithecus aethiops


<220>
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<221> misc_feature
<222> (1)..(891)
<223> n is a, g, c, or t

<400> 80
tttggtaact gtcagaccaa gttttactca tatcggatcc tctctatcag attgatctgc   60

aggtgagggt gtccagagat gtcttgcaaa tggcaatgtc ccaggccatg gaaacaggaa   120

tatgggctca aatccattta tggccaggca tggtggctca tgcctgtaat cccaacactt   180

tgggaggtca aggcaggagg attgcttaag cccaggagtt caagaccgtc tgggcaacgg   240

agaggagacc ctgtctctac aaataattaa aaaattatct gagcatagtg gcacatgcgt   300

gtggtcccag ctactcggga ggctgaagtg ggaggatcgc ttgaggccaa gaggtcaagg   360

ctgcagtgaa ctgtgatcat accacggcac ttgagcctgg cgacagagc aagaccctgt   420

ctttcttttt ttttttcaaa aaaaaaaat ccatttataa tttaacatgg gagcctcacg   480

ggaaagagtt cttgtcttgt tgagtggtcc agtgttttgg atgggctgga actttgcact   540

tgatgtgttg taattcattt tctagagtct atgtcgtgaa ggtccttggg gtgatagagc   600

cttggaaaaa tgttgtttcc ctgtggatta tctaaactag atccaagaac atgaaagacc   660

atccctcagg gagctggcat ttgtctaaaa accancattn cctgggccat ttgattgggg   720

ntcttgcttc actgcaaang ggggacttgc aaaattttac tnatgncccn nttgttnttt   780

ttntccaagg ggntttttana aaatttttct tnncnntttt ncnnaanacc ccnttnnant   840

tntntttttnc nnccccnttt nttntaacna ngggggggntt ttnaacnncc n   891

<210> 81
<211> 803
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(803)
<223> n is a, g, c, or t

<400> 81
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caactctctc ttcccacctg cccccaaac tcccttccac ctccctccac atgtatcctc   120

ccacttcctt ccactcatgt aatgagaggt gctgatgagt cacaggagag gtagccctag   180

ataaccaaca gactgcaaaa cggacagtcc ctggatgtct gagccagtgt ttgtgcactg   240

cattgactgg ctcctcgtag tttttttcctg tagttgctaa agcctgtaag gtctgtgtga   300

tgaatatttt ctaacacatc ttagaagaac ataatgcaag acagaatgaa aaactagaga   360

ggcagaaacc cccaaagtaa gtagtgggaa attaccaggt atataatagg tcaagcctgc   420

tctgcaggag ctcaagggat tgtagcattc ttatcccaaa ccactgaatc ctgggcaaaa   480

ataagaagtc gcctaatttt agtattacca gcttcccaac cccgggcatt cttcatctta   540

ctcaagctgt ccagaggccc cagggtgact ccctataagt cccatgggtg gctgagatct   600

atttagaggc acaagggtat ctccttataa gtcccatggg tggctgagat ctatgagaag   660

catcttgggg agagtgcctc tggccaccag catgtggccc tgaatctttc atgtgcaact   720

ggccagggaa ggaaattatg gaaatagtca tcctgcacat ntgcaaatga gatgcaaatc   780

ctggaagctc ttctaaaaaa aaa   803

<210>   82
<211>   763
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(763)
<223>   n is a, g, c, or t

<400>   82
tcgtgcttta cggtatcgcc gctcccgatt cgcagcgcat cgccttctat cgccttcttg   60

acgagttctt ctgagcggga ctctggggtt cgaaatgagc tagcccttaa gtaacgccat   120

tttgcaaggc atggaaaaat acataactga gaatagaaaa gttcagatcg aggtcaggaa   180

cagatggaac agggtcgacc ggtcgaccgg tcgaccctag agaaccatca gatgtttcca   240

gggtgcccca aggacctgaa atgaccctgt gccttatttg aactaaccaa tcagttcgct   300

tctcgcttct gttcgcgcgc ttctgctccc cgagctcaat aaaagagccc acaacccctc   360

actcggggcg ccagtcctcc gattgactga gtcgcccggg tacccgtgta tccaataaac   420

cctcttgcag ttgcatccga cttgtggtct cgctgttcct tgggagggtc tcctctgagt   480

gattgactac ccgtcagcgg gggtctttca gtagcccttc ctttgtagca aagacagaca   540

gatggtgatc caagagatac gcaagaagag gaccgtgtgt gtaatggttg agctctaaaa   600

agagaaatca cttggatgga aatgaaggag aggaaaaggc tgatgtggat ggctgggaag   660

aggttcgatg gttaccttgg caaccgagct tctttctcat cccatccctt ccctagtcct   720

tgtcttaaaa gatttttttn tatgtccctt ccctcccaag ggg   763

<210>   83
<211>   861
<212>   DNA
<213>   Cercopithecus aethiops

●

●

```
<220>
<221> misc_feature
<222> (1)..(861)
<223> n is a, g, c, or t

<400> 83
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tctagattga aatcacagat tttggataga gaaaaaaaaa tattctctgc aatctaataa     120

aaccaacttt tttttttttt tttttttttt ttgagacaga gtcttgctcc atggcccagg     180

ctagagtgca gtagcacgat ctcggcttgc tgcaacctct gcctgtcggg ttcaaccgat     240

tctcctgcct cctgtctcct gccccagcct ntcaagtagc agggattaca ggcatgtgcc     300

atgatgccca gctagttttt tgtattttta gtagagatgg ggtcttgcca tgttgcccag     360

gctggacttg aactcctgac ctcaggtgat caggccatct tggcctccca aagtgttggg     420

attacaggcg tgagccatcc tgcctggcca aaaccagcat attttatgga taggaaattg     480


gaccaaaggc gaatctttta ttgcaggctg tgggnttttt ccatgtggct ggtggnacac     600

tgcaccaagc agcacacaca ctaggccagt ttnctttgca gacccagttg caatcccatc     660

tntnagccag gattctatta ggtctcnaca accnatggga atttagggng ctcanagntt     720

nngggtggga aaaggggact aacctncntg ggttnanggn tttnnaantg gncncnncct     780

ttggancngg ganatttatt nccaaaanng gnngggntng tnttngggnn anaaaccaaa     840

ttttgggaaa aaancntttt t                                               861
```

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<210> 84
<211> 767
<212> DNA
<213> Cercopithecus aethiops


<220>
<221> misc_feature
<222> (1)..(767)
<223> n is a, g, c, or t

<400> 84
ggnattgncn agcggntaac aatttcacac agnaattccg tatttgaaat ttggggacaa      60


tcgcttgaat cttaaaatta cttttctggt cacgcgcgcc gaaggtctaa gcatttgtga     180

aatgtctttt ttcccccccc ccacccttg atgctgttct ctttgggctg tcttaattac     240

acaggggttg agaaaccaaa ttaaaattag gcgtgtctgg tcaacagtga tcacgttgca     300

tgcttttagc tttgcttgtt gaagttgctt ctcctccctg agtggctttc ctcctttttt     360

tttttttttt tttattttaa aaaggaaata tcataagctc tttcagaaat actcacagga     420
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agtgagtgtc cgtatgctgg ttactcacca gcaactgant gttggcaggt ggagaatgct   480

accgcanccn cccanacaga tctgcaaact ggcccnttnc agangatnaa aacagggtgc   540

gtggaantan ggtttttgnn naaangcant ttnaaagnaa atgggcactg cattnnnttc   600

naggggggg anttaagnaa cangnttggg gtnaaaaagn ncntgnttcc attnnggngg   660

tnctgctcct ttnaaanggg nggnnggttt naaaaaaaag ggccccncnc cccanaaaaa   720

aattttttgg nggaaaacct nccaaaaaaa anacccncn tttttgn   767

<210>   85
<211>   761
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(761)
<223>   n is a, g, c, or t

<400>   85
cngcttgcca acctacaggt ggggtctttc aaaatattgc gttacaaata tcattttggt   60

gtatgtatgt caaaaccaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat   120

atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca   180

tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg   240

cccttttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag   300

tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa   360

gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa   420

atgccaaatg ccagcgctcc ctttncccag ctcatcttat ttgtaggcac tcagattttg   480

gaatcctcca ggactaacat taaaaccca ctagggngtt tncctaatnc cgggaaanga   540

gncagtaggn caaacaactt atccccncna nanaggaaca attccttgag ctccccncct   600

gtttcngaaa ccctnttccc ttntgggncc ctgnanaagg nctgcccnaa tgctngggag   660

nccnccnggt tttnatgaaa accatntnaa aatncccnaa agttncccc ccaaggnaan   720

nttccnttta aanttttggg aaaaaaancc ccntnanaaa n   761

<210>   86
<211>   791
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(791)

60

<223>   n is a, g, c, or t

<400>   86
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cattttggtg tatgtatgtc aaaaccaaaa ctgcctttat gtcaatatgc tgtaaaaatc   120

tatcagaata tatcttaatt cttaactttc attgttgtct gtgggctgtc ttgtataacn   180

attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg   240

gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc   300

aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa   360

ggatcccaag cgcaggactt gtcctggaag cagaggatcg gattccacca ggaaaagagg   420

caagtagaaa tgccaaatgc cagcgctccc tttccccagc tcatcttatt tgtaggcact   480

cagattttgg aatcctccag gactaacaat aaaaaccaca ctaggttgtt ttcctaattc   540

ctgtgaaatg agtcagtagg tcaaacaact tatccactcc agagagagaa caattccttg   600

agctacactc cctgtttcca gtaaccctat tccctctctg tgtccctgga taaagtgctg   660

ncnacaatgc atgganagcc cccgggttct gatgaaancn atngaaagat ngcanaaagt   720

agctgcctta agggaangtt cccttngaaa tttaggnaaa aaaanccnnt aaaaanacng   780

gnggtcggtt t   791

<210>   87
<211>   783
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(783)
<223>   n is a, g, c, or t

<400>   87
ttgggganca gcttgccaan tctacaggtg gggtctttca aaatattgcg ttacaaatat   60

cattttggtg tatgtatgtc aaaaccaaaa ctgcctttat gtcaatatgc tgtaaaaatc   120

tatcagaata tatcttaatt cttaactttc attgttgtct gtgggttgtc ttgtataatt   180

attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg   240

gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc   300

aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa   360

ggatcccaag cgcaggactt gtcctggaag cagaggatcg gattccacca ggaaaagagg   420

caagtagaaa tgccaaatgc cagcgctccc tttccccagc tcatcttatt tgtaggcact   480

cagattttgg aatcctccag gactaacaat aaaaccacac taggtnggtt tcctaattcc   540

```
tgtgaaatga gtcagtaggn caannantta tncnctccag agagagaaca attccttgng    600

ctacactccc tgtttcnnna acccnattnc ctttctgngn ccctgganaa aggggtgccc    660

anaatgcntg gggnnncccc ccggntcttg annaaaaacn tnttaaaaan ngccnaaagt    720

ancctccntc nanggaagnt tccccttta aattttnggn naaaaaannc ccttnaanta     780

ann                                                                  783


<210>    88
<211>    769
<212>    DNA
<213>    Cercopithecus aethiops


<220>
<221>    misc_feature
<222>    (1)..(769)
<223>    n is a, g, c, or t

<400>    88
ttggnattgn ccagcggnta acaatttcac acagnaattc cgtatttgaa atttggggac     60

aaacaaacat aactctttct ctttccttga agggttaatg ctccaaccag cctcagattg    120

gttcgcttga atcttaaaat tacttttctg gtcacgcgcg ccgaaggtct aagcatttgt    180

gaaatgtctt ttttccccccc ccccacccct tgatgctgtt ctctttgggc tgtcttaatt   240

acacaggggt tgagaaacca aattaaaatt aggcgtgtct ggtcaacagt gatcacgttg    300

catgctttta gctttgcttg ttgaagttgc ttctcctccc tgagtggctt tcctcctttt    360

tttttttttt tttttatttt aaaaaggaaa tatcataagc tctttcagaa atactcacag    420

gaagtgagtg tccgtatgct ggttactcac cagcaactga gtgttggcag gtggagaatg    480

ctaccgcagc cgcccagaca gatctgcaga ctggccccat tgcagangat tagacacagg    540

gtgcgtggat catangggtt tttgtacaga aggcagtttt aagangaaan tgggcactgc    600

atgtcatctc nanggggngg tgattcangg ancanggctg ggggtnaaaa gcacctggct    660

gccattnngg agntcctgct aatttttaaa nggcagggtg gttttaaaaa aaaagctccc    720

ccccccccaa aaannnnttt tttggaggna naacttccaa aangaanga                769


<210>    89
<211>    754
<212>    DNA
<213>    Cercopithecus aethiops


<220>
<221>    misc_feature
<222>    (1)..(754)
<223>    n is a, g, c, or t
```

<400> 89

```
cagcttgcca acctacaggt ggggtctttc aaaatattgc gttacaaata tcattttggt      60

gtatgtatgt caaaaccaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat     120

atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca     180

tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg     240

cccttttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag     300

tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa     360

gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa     420

atgccaaatg ccagcgctcc ctttccccag ctcatcttat ttgtaggcac tcagattttg     480

gaatcctcca ggactaacaa taaaaaccac actaggttgt tttcctaatt cctgtgaaat     540

gagtcagtag gtcaaacaac ttatccactc cagagagaga acaattcctt gagctacact     600

ccctgtttnc agtaacccta ttccctctct gtgtccctgg ataaagtgct gcnacaatgc     660

atggggagnc caccgggttc tgaatgagac aatcgtaaan atngccaaaa nttagctgcc     720

ntcangggaa anttnccntt tgaaatttaa gnaa                                 754
```

<210> 90
<211> 866
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c, or t

<400> 90

```
tnggggaacc ctgnccagna ccttttttac tcatatccgg atcctgacct acattcagtg      60

ttctagattg aaatcacaga ttttggatag agaaaaaaaa atattctctg caatctaata     120

aaaccaactt ttttttttttt ttttttttttt tttgagacag agtcttgctc catggcccag     180

gctagagtgc agtagcacga tctcggcttg ctgcaacctc tgcctgtngg gttcaaccga     240

ttctcctgcc tcctgtctcc tgccccagcc tntcaagtag cagggattac aggcatgtgc     300

catgatgccc agctagtttt ttgtattttt agtagagatg gggtcttgcc atgttgccca     360

ggctggactt gaactcctga cctcaggtga tcaggccatc ttggcctccc aaagtgttgg     420

gattacaggc gtgagccatc ctgcctggcc aaaaccagca tatttatgg ataggaaatt     480

gaggcttaga tggggggaga aaaacattac acagattaaa ccacagctaa tgtcaagtgg     540

tgaccaaagg cgaatctttt attgcaggct gtgggttttt ccatgtggct ggtggtacac     600
```

```
tgcaccaagc agcacacaca ctaggccagt ttcctttgca gacccagttg caatcccatc    660

tntaanccag gatactatta ggtctcnaca ncctatggna ttttagggtg ctcanagttt    720

agggtgggaa aaggggacta anctncttgg nttaaggtnt ntccactggn ccctcncttt    780

nggnccnggg antttnatgc ccaaaancgg tngggctttt ttgggggnan aannccaanc    840

cnngggaaaa aaacnttttt gttang                                         866
```

<210> 91
<211> 783
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(783)
<223> n is a, g, c, or t

<400> 91
```
tgggnntgnc cagcggntaa cantttcaca cagaattccg tatttgaaat ttggggacaa    60

acaaacataa ctctttctct ttccttgaag ggttaatgct ccaaccagcc tcagattggt    120

tcgcttgaat cttaaaatta cttttctggt cacgcgcgcc gaaggtctaa gcatttgtga    180

aatgtctttt ttccccccc ccacccccttg atgctgttct ctttgggctg tcttaattac    240

acaggggttg agaaaccaaa ttaaaattag gcgtgtctgg tcaacagtga tcacgttgca    300

tgcttttagc tttgcttgtt gaagttgctt ctcctccctg agtggctttc ctcctttttt    360

tttttttttt tttattttaa aaaggaaata tcataagctc tttcagaaat actcacagga    420

agtgagtgtc cgtatgctgg ttactcacca gcaactgagt gttggcaggt ggagaatgct    480

accgcagccg cccagacaga tctgcagact ggccccattg cagaggatta gacacagggt    540

gcgtggatca tanggttttt gtacagaagg cagttttaag aggaaattgg tcactgcatg    600

tcatctcgag gggtggtgat tcaaggagca gggctngggg gtcanaangc acntggctgc    660

catctcgggg gttcctgctc acttntnaaa gggcaggctg gcttntaaaa anaaatgctn    720

ccttcacccc caaanaggga ttttttttgc agngaataac ttcccaaaaa tgaatngccc    780

cna                                                                 783
```

<210> 92
<211> 775
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(775)

<223> n is a, g, c, or t

<400> 92
```
ttggggaanc agcttgccaa anctacaggt ggggtctttc aaaatattgc gttacaaata    60

tcattttggt gtatgtatgt caaaaccaaa actgccttta tgtcaatatg ctgtaaaaat   120

ctatcagaat atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat   180

tattatcaca tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag   240

ggggaaaatg ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag   300

caagaactag tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa   360

aggatcccaa gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag   420

gcaagtagaa atgccaaatg ccagcgctcc ctttccccag ctcatcttat ttgtaggcac   480

tcagattttg gaatcctcca ggactaacaa taaaaaccac actaggttgt tttcctaatt   540

cctgtgaaat gagtcagtag gtcaaacaac ttatccactc cagagagaga acaattcctt   600

gagctacact ccctgtttcc agtaaaccta ttccctctct gtgtccctgg ataaagtgct   660

gccaanaatg catggagagn cccccgggtt ttgaatgana cccatcgtaa agatngccaa   720

aagntagctg ccttcaaggg aagttnccnt ttganattta gnagaaaaag tccnt          775
```

<210> 93
<211> 837
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(837)
<223> n is a, g, c, or t

<400> 93
```
ttnggggganc tagcttgcca aanctacagg tggggtcttt caaaatattg cgttacaaat    60

atcattttgg tgtatgtatg tcaaaaccaa aactgccttt atgtcaatat gctgtaaaaa   120

tctatcagaa tatatcttaa ttcttaactt tcattgttgt ctgtgggttg tcttgtataa   180

ttattatcac atctacagta ttttctgtag gtaaatatga aatgtattat aaatgtacca   240

ggggggaaaat gccctttaat aagcctttcc ctagacaaag caccatttag gcgtttagaa   300

gcaagaacta gtgaaatcag aaattgctgt catacatact cacctgtgaa tggtcgtaca   360

aaggatccca agcgcaggac ttgtcctgga agcagaggat cggattccac caggaaaaga   420

ggcaagtaga aatgccaaat gccagcgctc cctttnccca gctcatctta tttgtaggca   480

ctcagatttt ggaatcctcc aggactaaca ntaaaacccc actagggggn ttncnnantc   540

ctgngaaatg agtcagtagg ncaaacannt ttncnctcca nanannnaan antccntggn   600
```

ntacnctccc tgnttcagna acccnattcc ctncntgggn ccnggnaaaa gggcgnccca   660

aatggnnggg ngnccccgg nttntnanga aacccatnnt aaaattnccc aaaantttnc   720

nccccnnann gaaannnncc nttttaaatt ttngganaaa aaancccnt naaaaaaana   780

nggggcggn tttnttttn aaagaaanaa anatttttt ttnnggagg ggttnnt   837

<210> 94
<211> 837
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(837)
<223> n is a, g, c, or t

<400> 94
ttggggnacc ctgncagncc antttactc atatcggatc ctgacctaca ttcagtgttc   60

tagattgaaa tcacagattt tggatagaga aaaaaaaata ttctctgcaa tctaataaaa   120

ccaactttt tttttttttt tttttttttt gagacagagt cttgctccat ggcccaggct   180

agagtgcagt agcacgatct cggcttgctg caacctctgc ctgtcgggtt caaccgattc   240

tcctgcctcc tgtctcctgc cccagcctct caagtagcag ggattacagg catgtgccat   300

gatgcccagc tagttttttg tattttagt agagatgggg tcttgccatg ttgcccaggc   360

tggacttgaa ctcctgacct caggtgatca ggccatcttg gcctcccaaa gtgttgggat   420

tacaggcgtg agccatcctg cctggccaaa accagcatat tttatggata ggaaattgag   480

gcttagatgg gggggaaaa ancnttnccc aaattaancc acagcttatg tnaagtggtg   540

gncccaggcg gnccnnnctt tggnccnttt tcttttggaa cccngntgca atcccctttt   660

taanccggga atctttggg tttcncnccc cttgggnatt nnggggggccc caanttnngn   720

nggggnaagg ggnaaaaacc ccttggntn agggntttaa aangggnccc ccctttggnc   780

cnggnntt tntnccnaan ngggnggggt ttttttgngg annaacncnn acnnggn   837

<210> 95
<211> 812
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(812)
<223> n is a, g, c, or t

<400> 95

```
ttggggttgc gagcggntaa cantttcaca cagaattccg tatttgaaat ttggggacaa        60

acaaacataa ctctttctct ttccttgaag ggttaatgct ccaaccagcc tcagattggt       120

tcgcttgaat cttaaaatta cttttctggt cacgcgcgcc gaaggtctaa gcatttgtga       180


acaggggttg agaaaccaaa ttaaaattag gcgtgtctgg tcaacagtga tcacgttgca       300

tgcttttagc tttgcttgtt gaagttgctt ctcctccctg agtggctttc ctcctttttt       360

ttttttttt tttactttaa aaaggaaata tcataagctc tttcagaaat actcacagga       420

agtgagtgtc cgtatgctgg ttactcacca gcaactgagt gttggcaggt ggagaatgct       480

accgcagccg cccagacaga tctgcagact ggccccattg cagaggatta gacacagggt       540

gcgtggatca tagggttttt gtacagaagg cagttttaag angaaattgg tcactgcatg       600

tcatctcgag gggtggtgat tcanggagca gggctggggg tcanaangca cgtggctgca       660

tctcggnggt nctgctcant tttaaagggn ngctggnttt aaaaataang ntncttcacc       720

ccaaaangaa tttttgcag gnaaanttc naaaaganna cccnantttt tgnnaaaacn          780

tgggaaancc ccntttnaan ggnggnttta an                                     812
```

```
<210>  96
<211>  805
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(805)
<223>  n is a, g, c, or t

<400>  96
```

```
ttggggancn gcttgccaan tctacaggtg gggtctttca aaatattgcg ttacaaatat        60

cattttggtg tatgtatgtc aaaaccaaaa ctgcctttat gtcaatatgc tgtaaaaatc       120

tatcagaata tatcttaatt cttaactttc attgttgtct gtgggttgtc ttgtataatt       180

attatcacat ctacagtatt ttctgtaggt aaatatgaaa tgtattataa atgtaccagg       240

gggaaaatgc cctttaataa gcctttccct agacaaagca ccatttaggc gtttagaagc       300

aagaactagt gaaatcagaa attgctgtca tacatactca cctgtgaatg gtcgtacaaa       360

ggatcccaag cgcaggactt gtcctggaag cagaggatcg gattccacca ggaaaagagg       420

caagtagaaa tgccaaatgc cagcgctccc tttccccagc tcatcttatt tgtaggcact       480

cagattttgg aatcctccag gactaacaat aaaaaccaca ctaggttgtt ttcctaattc       540

ctgtgaaatg agtcagtagg tcaaanaact tatccactcc agagagngaa caattccttg       600
```

```
agctacactc cctgtttcag naaccctatt ccctctctgg gtccctggat aaagggctgc        660

cacaatgcat ggggagcccc cnggntnttg atggnaacac tcntaaaaat tgccaaaagn        720

tnnctgcctn aangaaaant nccctttnaa tttttggana aaaaanccct tnaanaaacn        780

gggggcggt ttttcnttaa agaaa                                              805
```

```
<210>  97
<211>  854
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(854)
<223>  n is a, g, c, or t

<400>  97
ttggggaacn ngcttgccaa ntctacaggt ggggtctttc aaaatattgc gttacaaata         60

tcattttggt gtatgtatgt caaaaccaaa actgcctta tgtcaatatg ctgtaaaaat         120

ctatcagaat atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat         180

tattatcaca tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag         240

ggggaaaatg ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag         300

caagaactag tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa         360

aggatcccaa gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag         420

gcaagtagaa atgccaaatg ccagcgctcc ctttccccag ctcatcttat ttgtaggcac         480

tcagattttg gaatcctcca ggactaacaa taaaaaccac actaggttgn tttcctaatt         540

cctgtgaaat gagtcagtag gtcaaacaac ttatccactc cagagagaga acatttcctt         600

gagctacact ncctgnttcc agtaacccta ttccctctct gggtccctgg ataaagggct         660

gccnacaatg catngggggg cccccgggt tntgaangaa aannntnntt aaaaatngcc         720

aaaanntaac tnccctcaan ggnnannnnc cccttttnaa ntttttgggn aaaaaaaanc         780

cccntnaaaa aananagggg gggnggnttt ttttttnnaa aanaanaann aanntttttt         840

tttggggnan annt                                                         854
```

```
<210>  98
<211>  912
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(912)
```

<223> n is a, g, c, or t

<400> 98
ttttgttgtt ggggnntgna gcgncggctn aacttttttg cacacagaaa ntcacaggaa   60

cacaggagtc agtttcttca gcaangtctt gcttgtccng ttntgaacgg taggatnttg   120

tcgctatatt tgnacacatg agggacctnt gtggagcttc caaatagtgc gctnggcgca   180

atatnnacaa ganacagccc ttagcgantg gcttgttgnt gggngagatg ntgctctgtg   240

ngatgaattn acanatcaca gagtttttn tttgnntgct tgtttcctgt tntnaacggt   300

ggatttgtgn ttttggacca tgggatntct atgggctnan agangtccta tgtgngaata   360

nggcaatgta ctgcctttna naactggaat gangctnggt gagaanctgc tctgtgttct   420

gtganttccg tactntgaaa tttggggacn aacaaacata nctctttttt cttttccttg   480

aagggntaat tgctccaacc ccgccncaga ttgggntngc ttgaatctta naattncttt   540

tctggtcccg cccgccgang gntnagcttt tgngnaaatg gtnttttttc cccccccoca   600

ccccttggtg gngggtnttt ttgggcttgg nnttnanntn cccccggggg nntngnnnna   660

ccnattttnn attttgggnn nttttgggnc ncangggttc cnnnnnnnnn gnctntnann   720

cttggcttgn nngaangntg nttntccccc cccggggggg ttcccccont tttttttttt   780

tttntttttt tttnnagggg antttntntg tcttttnna anncncncgg gntgggggn   840

tcnntttttt gttttnncn nnnnttggnn nnggggggg gganntttct ctnnnnoccc   900

cnnnntttnn gc   912

<210> 99
<211> 807
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(807)
<223> n is a, g, c, or t

<400> 99
ctgcttgcca anctacaggt ggggtctttc aaaatattgc gttacaaata tcattttggt   60

gtatgtatgt caaaaccaaa actgccttta tgtcaatatg ctgtaaaaat ctatcagaat   120

atatcttaat tcttaacttt cattgttgtc tgtgggttgt cttgtataat tattatcaca   180

tctacagtat tttctgtagg taaatatgaa atgtattata aatgtaccag ggggaaaatg   240

ccctttaata agcctttccc tagacaaagc accatttagg cgtttagaag caagaactag   300

tgaaatcaga aattgctgtc atacatactc acctgtgaat ggtcgtacaa aggatcccaa   360

gcgcaggact tgtcctggaa gcagaggatc ggattccacc aggaaaagag gcaagtagaa   420

```
atgccaaatg ccagcgctcc ctttncccag ctcatcttat ttgtaggcac tcagattttg    480

gaatcctcca ggactaacan taaaacccca ctaggttgnt ttcctaattc ctgtgaaatg    540

agtcagtagg tcaaanannt ttncnctcca ganaggaaca attccttgag ctanctccct    600

gtttcaggaa ccctattccc ttntgggncc ctggaaaang gctgccacan tgctgggaag    660

ccccgggtt tnaangnaaa aatcnnaaaa ttgccaaaan tancnncccn agggnnggtn     720

cccttanant tttnggaaaa aanccccnta aaaaancngg ggncgnnttt tnttaaaana    780

aaanaaattt ttnttngggn gntttnn                                        807
```

<210> 100
<211> 814
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(614)
<223> n is a, g, c, or t

<220>
<221> misc_feature
<222> (1)..(814)
<223> n is a, g, c, or t

<400> 100

```
ttggnattgn ccagcggnta acaatttcac acagnaattc caggcacagt tggctgttaa    60

ctagaatagt aagtggcttc ctaggctctg tcactcctaa actgtagggg gcttccagcc    120

tcggagatta cggaagtagt acttttcatt agcaagctca agaagaagtg tcaaaatagg    180

atgacacttt cctagtcgct ctgcaaaaac ccaaaaaacc agaaggggtg tcatctagac    240

actcctaagt ctatgcaggt gtcagcctgc cctcacccaa caccagccag cagcgtgcac    300

cattcaacca tatcttaact tgcccttac aaattgacac ttacactaac aagcccttg    360

atctcatttg tttaaaatga cagatataca accctcacgg gggttccac tcaaggcctt    420
ncagcctncg ncctgcccct gnccacccc aaacctacac acgtgttagc ccgacaccgg    480

ccccaccggg tcccacgtgc acctggtcta acacactncc cacgtgtggg cgccccacgg    540

gctttctnan gtagctgang gnccccccat gatccccggt tntccaaaan aaaaaaacgg    600

gaaggacaag ggcccttttc nccgnggncc caaccntngg ggggggnggt ccaacccctt    660

tnttnnntat aaaccccaaa aaananaaag ggcccggggn ccnnccccc ccttnaaaaa     720

ncccgncccc cnttttncc cccnaaaaaa nggggggaaa aaaaaaattt aaaaaaannc     780

ntttttttnt tttnncccc ccnncatnta nata                                814
```

<210> 101

<211>   756
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(756)
<223>   n is a, g, c, or t

<400>   101

tggtcccaga gtctaaatag gagccccaaa ctaatcactg tatggtagtc gaacttcccg   120

gcacttcccc gacaatctac aaccccatcc aaaggggtca gaaactggta ataaaatacc   180

agctatgagc ctntccttcc cctcaagaga tctatcaatt cggcctcacc ttcccacctc   240

tagcctgcgg gaacaaacat cccaggatcc cgggcggttt cgattgacgt tacttccggg   300

aaaagtaacc ttgcttcggc ggttgcgggc ctgaaaagct ctcgcgacat ttcctcccgc   360

nagatctgct tgctcactgt agcgatgaca tcctcctcct cctccccgcc gcctttcggc   420

aatcttcgcc agtcccagcc ccgaccaatc tgtactcaga tggcatggat cagggtctcc   480

cctcgaaccc cggttcgcac ggggcgtcag gtggcagcgg cggggtgcga gctgcgcgag   540

gccnacngca gcggcactgc gggtggccng gggcaggcca caagcantga ntgtnggccg   600

ggccgggggn aacccacccg ngtagcggct cnantgnttc tggcctggct ttngngccct   660

tttctccccc ccncangggt tcccgggnnc ctgttncgnt tctttaann ggggaaaggg   720

gcccccccc ccccngnéca angccccnnn acnnnt   756

<210>   102
<211>   804
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(804)
<223>   n is a, g, c, or t

<400>   102
tgggntgncc agcggntaac antttcacac agaattccaa ttatggggaa caagacatct   60

gaattggcta aaactccttg cagcagcaaa aaggaaaagc aaaacaaaac catacatgtg   120

gtttctgtct ttgcttcctg tctttttcttc caccttactc ctccttcccc ttccccttcc   180

ccttcccctt ccccatcttt gctaccaaaa aaaaatctag agaagccttc tattaacctg   240

aacccctaa agaagtcaga acaaaggcac cacttgccgc tttttgggat gtcgtgtttt   300

ctttatggag ttttcaagag taatgggcag atgctttag gtctacagtt ctgcttcct   360

```
gtattgcact acctgattct ttgacttttg gagataccag aaattacctt gtaccatgag     420

aggatttggc tttggcatgt gtaatggcag atgagagcta caaagttaag agtggctgaa     480

gatggtttac atgaagtggt cttaggtggt ttagctgagc tcccaggaag ttgttgtcta     540

ggatcccaat tctagttcag aggtgcattc ctattattat tatcattact attggtggtg     600

ntgntattat tttgagacag agtcttgctc tgttacccca ggctggagtc ctctggcacc     660

attacgggtn actggagcct naanttccag gctncagaga tcctcctttt annttcnnag     720

tagtgggacn canangnngg nnccccccaa cnnannnatt tttgnncttt tgnaanaann     780

gggtttgntt tttngncnnn ntgn                                            804
```

```
<210> 103
<211> 795
<212> DNA
<213> Cercopithecus aethiops


<220>
<221> misc_feature
<222> (1)..(795)
<223> n is a, g, c, or t

<400> 103
ggnattgncn agcggntaac aatttcacac agnaattctg gagttaggtt gtctgggcta      60

ttcaattagt ttctatgtgt ctgacacatg gcagaaactt attaaatgct tgaatgaata     120

cataaagcaa gatgacagtt tcagaatgna ccaggtaatt caaagtactg aatccatatt     180

aaatttattt tagtctacac agaagtgaag taacactaaa atctgggcat ttaccaggtg     240

atggcaagta ttcatttcca tcatccagcc cgttacctgg cacatagtta ctgccctatg     300

taaatgctta tcacagcaat caatcaatga aatgtttttc tcatagagtt cggtgaataa     360

ctcacgacag catactcaca gaggattcaa agagtatttg acttgtatat attgttttaa     420

acagttggaa cctgataatg cagttttcta aaatacagtg aaagggcttg tcctaaaggg     480

catgtcagga tatgtgtgag aaaggatgaa cttgtcctgt gaagacaacc ttgcattagc     540

tctagcagaa tgagccattg cctacctggg ctggggaagg cggcacctca gtatctccct     600

cacctgctcc ctggcacttt aaatccctct gtgaagangt cagttgtaat tttcagtaag     660

attgaaggtt tcaaagcact gacccctggg gggaatggat tngcttaagt tggctctgaa     720

ngaagnggct gggatnngct ntctganaaa cccgggattg tgaggnaatg gagacngccg     780

ggagggtnna anaaa                                                      795
```

```
<210> 104
<211> 641
<212> DNA
```

<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(641)
<223>   n is a, g, c, or t

<400>   104

```
tggggggnacc cagcggntaa cattttcaca cagaaatctc attcaatgaa ctgttatggg       60

gtctcacatt gtaccaggca ctggggattc agcttccagt tcatagtctg catgcaaacc      120

gacatgcagg tagacatgca gacagaaaat cggaacgcaa cacggtaagt gctatgctag      180

agaatgagaa ggactgtcag taatcacaac cacctttcac tgggttcctt cagtgtgcca      240

ggctcgtgta cattattttg tttagtgctc acaattgtat ggactgtgta ctatcatttg      300

ccagattata tggatgaaga aactagactg aggggggttaa ataactcgtc caagatcatg      360

cagacaaaaa accacagaga ttattttcca atacaaactc tctggctgta cagctcaagt      420

tcttaaacac tgggccaacc agtctgaatc tgagaggagg cattctaagg cttacaggta      480

agtgggaatt gaaagggttg agggaagcct tctggaggag atgccattac actgaatgtt      540

gaatgagtag gagttagcta tctccagagg ggtagtggct gtgaaggggc gaggggtana      600

gggtgggaag gggatgatgg aaggtggtag agtggnnaca g                          641
```

<210>   105
<211>   757
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(757)
<223>   n is a, g, c, or t

<400>   105

```
cngncttgcc aacctacagg tggggtcttt caagatctgc tgacagtgaa gctaaatctg       60

gcggaagcaa aggattcact ttctcataat ggattaactc atcctatttg cctcttaaac      120

aatgggtatt ttaaagacag aagttgaagg aagtccaagt atccaatttt aaggatgcct      180

attagagcag ttataagaga gtgtctctct ttctctctct tctttctttc tcttggtagg      240

agtatgcagg aggtcattta aaagccagat agtgatacaa atcacaatgc agaaaaacat      300

ccccgtggac tcctccctgt cctatgtttg acattcttaa aatctatgtc ccaggtcttg      360

aaatctttaa ataatctacc atgttctttg gcctgccctg ggaaatctat ttcagtacca      420

gagctatgct ggttacacac cttttctgac tcatgttccc aagtgatttt attccagata      480

cgatttgggg acagttacgt gtactgttct gatatcttcc taaaaggaaa ttatttttgg      540
```

73

aagtaaagtc actgataaaa tcanctcagg aaaatgcact ttgtaaatat taaaatataa   600

actttttnaa ggncntgctg gaaaanacta attgattttc ctgggnagca gttccatnga   660

acancgatng atctttaggg ggnagtgaan ggccccnatt tgaaaaangg gggcgggaaa   720

ngttcaaata ntttttccaa angggnncct anntnnt   757

<210>   106
<211>   640
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(640)
<223>   n is a, g, c, or t

<400>   106
ttggggnanc gagcggntaa catttcaca cagaaattca ttcaatgaac tgttatgggg   60

tctcacattg taccaggcac tggggattca gcttccagtt catagtctgc atgcaaaccg   120

acatgcaggt agacatgcag acagaaaatc ggaacgcaac acggtaagtg ctatgctaga   180

gaatgagaag gactgtcagt aatcacaacc acctttcact gggttccttc agtgtgccag   240

gctcgtgtac attattttgt ttagtgctca caattgtatg gactgtgtac tatcatttgc   300

cagattatat ggatgaagaa actagactga gggggttaaa taactcgtcc aagatcatgc   360

agacaaaaaa ccacagagat tattttccaa tacaaactct ctggctgtac agctcaagtt   420

cttaaacact gggccaacca gtctgaatct gagaggaggc attctaaggc ttacaggtaa   480

gtgggaattg aaagggttga gggaagcctt ctggaggaga tgccattaca ctgaatgttg   540

aatgagtagg agttagctat ctccanaggg gtagtggctg tgaangggcn aggggtaaag   600

ggtgggaagg ggatnatgga aggggtnnaa tnggnncnng   640

<210>   107
<211>   818
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(818)
<223>   n is a, g, c, or t

<400>   107
ttggggacca gcttgccaat tctacaggtg gggtctttca agatctgctg acagtgaagc   60

taaatctggc ggaagcaaag gattcacttt ctcataatgg attaactcat cctatttgcc   120

74

```
tcttaaacaa tgggtatttt aaagacagaa gttgaaggaa gtccaagtat ccaattttaa    180

ggatgcctat tagagcagtt ataagagagt gtctctcttt ctctctcttc tttctttctc    240

ttggtaggag tatgcaggag gtcatttaaa agccagatag tgatacaaat cacaatgcag    300

aaaaacatcc ccgtggactc ctccctgtcc tatgtttgac attcttaaaa tctatgtccc    360

aggtcttgaa atctttaaat aatctaccat gttctttggc ctgccctggg aaatctattt    420

cagtaccaga gctatgctgg ttacacacct tttctgactc atgttcccaa gtgattttat    480

tccagatacg atttggggac agttacgtgt actgttctga tatcttccta aaaggaaatt    540

attttggaag taaagtcact gataaaatca actcaggaaa atgcactttg taaatattaa    600

aatataaaca ttattaaagg ccatgctgta aaaatactaa ttgattttcc tgggtagcag    660

ttacaataga acancgatng atctctaagg ggagagtgaa aggacctcan tttganaaac    720

gtgaggcagg aaaagnttca aatnattatt tncaanaggg ntccctaagt tgttncttaa    780

anaaaatttt tttcntnaaa aaaaaacnnt aanggcca                           818
```

```
<210>  108
<211>  608
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(608)
<223>  n is a, g, c, or t

<400>  108
ttgggaccct gtcagaccan ttttactcat atcggatccc ctgaggtcgg gagatcaaga     60

ccaccctggc caacatggtg aaaccctgtc tctactaaaa tacaaaaatt agccaggcgt    120

ggtggcaggc gcctgtaatc ccagctactc aaaggctgag gcaggagaat cgcttgaacc    180

taggaggcag aggtggaagt gagccgagat cataccactg cactccagcc tgggcatcag    240

agccagactc tgtcgcaaaa aaaaaaaaaa aaaaaaaaaa attagctacc tctccatcc    300

anaaatgaga gtcgaggctt ctgacttccc gggctcaatt tatcctcccg cctcagcctc    360

ttgaggaact gggactacag acgtgcacta tcacacttgg ctaatttttt tgagatgatg    420

tcttgctctg tgcccaggct ggagtacagt gacacaatct cagctcactg caacctccgc    480

ctnctgggtt caaccgattc tnttgcttca gcctcccaag tagctgggat tacaggcgtg    540

ccccacaacg tccagntatt tttgtatttn aagnagagac nggggnnncc cctgttggnc    600

ngggnggg                                                            608
```

```
<210>  109
```

<210> 516
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(516)
<223> n is a, g, c, or t

<400> 109
ngggancctg nccagnacct ttttactgca tatcggatcc tgagaagctc ctgattttcc   60

ctcaagccta aggcaaagta gtattcagaa cctcctatcc cactgactcc gagagcctgt   120

cctccgatat ctccaagaga gcctatcctc cgataggagg ggaagcccct ccaacctgca   180

ggtatcctcc ccagactcac catttctccc acccacact ggtggcttcc aaactttccc   240

tctcataaca aggcgccctg tcacccagac tgcttccctc ggcttgagga ggaggggaag   300

gcgcacgaag taggaaggaa cttggggaga gggcgggcgg agggtgggcg aagcactgag   360

gggagggcgg tgaagaaggc agaagtcagg cagtgagagg gagaagcggc ggggcaggt   420

gagggcgggg gagtggggat ggggccgggg aaaggggccg agaggacgcg gaggggcag   480

aggtagggna caggagggga ggggaggggg agggcc   516

<210> 110
<211> 802
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(802)
<223> n is a, g, c, or t

<400> 110
tnggggaacc tgccagacct tttttactca tatcggatcc ttattgcctg gctatttcag   60

cctgggaggg gtttggctgg aatatccctg gggaggcagg ctctcagggc taaaatagtg   120

ggagaaaaga ttaaaccttt aggaaactgg tacacatcag cgctaagtgt gactcaggga   180

gaaacaagaa ctaggacact tattactcca aaggagttgt atttggttca actcttgtat   240

tttcttatta aaactttgc aaagtgggtt gagaagaaag tgttacttcc agtgttacac   300

cctcaacact ttttcctgtg gagactccag catgttcatt atgttttctg aagccatggc   360

actgtagtac tcttttcattg ttgttattat tatttaataa tataaaatga gacattttttg   420

ctccattttt cattcatatt tttgtcctaa ttacttttta aatatattct ggtgtcaggt   480

caatatttat agtctaacgt ttaagactta gactttggtt cttaggatgt tatttttgaa   540

tcagctgcgt ctggtaaggt aatagatatt gaaagtgcct tgtaaattgt ccagtggcat   600

```
aaaagtattg tcatatcttt atgacataaa agaaaantgt tttcttcttt ttagcatgga      660

aaactttaca anccatttgc tggtgacngg ngangncctn ggggttggat ttcatgattt      720

tggggtccct tgagggtcca aantaccntt ctaanagngg aaanttttca nnaattcatg      780

antgncctna ttnaaanann tt                                              802
```

```
<210>  111
<211>  851
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(851)
<223>  n is a, g, c, or t

<400>  111
tacttttttt tggggggnncc aagncggnta acattttcac acagaaatct ccaagttccn      60

naggaccgca gnatcctccc cagaacccct gngaccaagt cactgtggtt ggntgtgctg      120

ggcatccctg aggcccagcc actcaacttt actggctcca ggattctata gaaagggaaa      180

ggggtagaaa atctcaaaag gcttcttcct ttcagggagg gggttccctc tcagcggctt      240

ctggaatctc tacccactcc agccgacttt tgaggccatg tggtcctgga acaaggcccc      300

tctgagggcg gcagatgggg caggcggccc aggcacacag catggttggc tctgcggccc      360

agggcccaca aaagccttat tgagtcacca ccagcccccg gcagaggctg aggtggcagt      420

ggcgccgagc gcctgccacc taatgactgt cctggcacag ccagatgttc cgcagacctc      480

cggagcagcg ggaccaaggg cccgcccggg ccagccggca ccngannagg ccacttttaa      540

tttccaatta accagntttc agnntgancn aaanaggggg gcagtnggtg gncccacccc      600

cgggcnagta ngccccggcc cnnaaaannc cttncgaagt tntaanactn ccanatntga      660

aaccnccacc ncccngaatt cccnatggaa aaantggccc ccagccangg gcaagggntt      720

gggncctttc ttttctttgg aaaaggaaat tttggttntt ttnacnaagg ccccccaang      780

aacccnatt t                                                          851
```

```
<210>  112
<211>  773
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(773)
```

<223>   n is a, g, c, or t

<400>   112

```
cagcttgcca antttacagg tgggantctt tcaagagcag taaaacgacc tatccaagga      60
aactcagcta gtaaaggcag ggacagggta tcgcaggctc tcggaactca cgagtccccg      120
ccaggcgcat ggccgctcct ttcccccggt gggcgtggcc aggccaggcc cgtcccctcc      180
cctgagcgcg ttcctggcag cccggccggc cgtttnctgc ctgcgtcgct gggcgcgcgg      240
gcgggcgggc agcccatctg gcggcccccg cggggcggcg cggggaggcg gcccagactt      300
gctggagcca ggcgcctgcc cggggggcccc cctgcccgcc tggagaaccc aggtgtggcc      360
gcggcggggg tggggggtgg tgctttcctt cccgctcgct cggctcttnc tgacgcacga      420
gggcaggatg cagcctcctc ccgtcctctc ctcggcctcc gcctcccgcg ccctggcccg      480
gaatcctgga gggaatccaa acgcggggcg gggaggccgg ggcaggcccc tgaggcccg      540
cccctgatag ccatttaata ccaccgcaag tcttgaccgt attttggggg tgacccanct      600
tccctgcttg ggcaagacca gctgaactct gacctnctgg anggccgatt ttaccttgct      660
cctcagggac ccnnaaatga tcgtaggaac cngnntcact actgctgtaa gccanancgc      720
ttganatatn caattattca gcggnttcaa gtcccggaag cggntttna cna            773
```

<210>   113
<211>   807
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(807)
<223>   n is a, g, c, or t

<400>   113

```
ttggggttgc gagcggntaa cantttcaca cagaattctt cagtgaattt cttaagccct      60
gagcatcttc tttgtattct gctttaagaa cttgtttgtt tctgtatttc atactcagtg      120
gctctggcgc ttggatgccc tggtcccaca gaaggccttg aatactgaat ctgaggatgg      180
ggcttgctta taggaccttt actccctgtc ttaaccagat tgtgttttaa cctttcatct      240
cacttttac ttttcattca tggatagtgt ttgtcactgt gtgtgtgtgt gtgtgtgtat      300
gaatgagtga atgaatatct ctcacactct aaattctttt aaaggcagga agtactgttc      360
tcttgtttgc tattttatcc actctgcctc tactgggtct ggcacataat aaagaaagaa      420
tgaacaggac aaacacccat tctgaaagtg aacttctctg gcaattgtcg tttgtacata      480
ccagctggag catagacaat tggcttttaa tgtggtaagg gaaaaggtca aaaaaagaat      540
cgtcattgac caagggcttc accagatgat tttataatca ntccnaaagg gnctttnaan      600
```

```
aaaaaaggcc ttngaggaac aaatttnttc cnnntggaaa antgntttna aatttttntn     660

gaaaaagttt tnanaatttt tgnaaaaccc ccnccccnnt gaaaacntnt aaancnngna     720

annngnnnng ggcggggttt naaaaaaaaa aantnccccc cnnnnaanng ggnctttnaa     780

aaannnnngn ntnctaaaaa aangggg                                        807
```

<210> 114
<211> 836
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(836)
<223> n is a, g, c, or t

<400> 114

```
ttggggacca gcttgccaan tctacaggtg gggtctttca gtatgtgtca agagtcagaa      60

tttaaagaag ataagaaat  taaatacact gagaacaatg catctcntga cattcaaaat     120

atgtaagtgc agcaaccagc agtaattcca taggcctttt atcaaccttt gccaaaacct     180

ataaaagaa  tatctaaaat tgctttttta tgaaagttcc tatttattct tgtttccctt     240

accagagagc ctgctttccc cttactgatg agaacacagg gggtcctggg taaagagtcc     300

ataanattta aaaaggagta tgccttggcc tcccatgacc ctcttacttc acaataaggc     360
catcttttac ctggtttaga tttgcagact aggtccatta gatacgttgt cattaaatac     420

ctatactata ccctaatatt tgtaatcttg acaggtatta ttttcatttt atagacagat     480

ctaggaaaat tacatgactt atcggaatcc cttcaaatat cacagagcaa agtcatgatt     540

ttaacttgtg tttgccactc tgaaactcac actggaattc gagactagtg tgcgtaacat     600

ggcgaaaccc catctctatt tnttnttttc aaaatntntt tttccaaaat ttgctggggg     660

tgttggtgtg tgcctgtant ncagcctnct tgggaggctn aannggngga cngcttgacc     720

ctgggngnaa aggctaaatn gnctttnttn gcccctggan ttaaccnngg ggaaaaangg     780

acccttntc  aaaataaatt ttaaattaaa naangccnag gtttccccna aaaat          836
```

<210> 115
<211> 839
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(839)
<223> n is a, g, c, or t

<400> 115

```
ttgggananc gagcggntaa cattttcaca cagaantcca gtgtgagttt cagagtggca        60

aacacaagtt aaaatcatga ctttgctctg tgatatttga agggattccg ataagtcatg       120

taattttcct agatctgtct ataaaatgaa aataatacct gtcaagatta caaatattag       180

ggtatagtat aggtatttaa tgacaacnta tctaatggac ctagtctgca aatctaaacc       240

aggtaaaaga tggccttatt gtgaagtaag agggtcatgg gaggccaagg catactcctt       300

tttaaatttt atggactctt tacccaggac ccctgtgtt ctcatcagta aggggaaagc        360

aggctctctg gtaagggaaa caagaataaa taggaacttt cataaaaaag caattttaga       420

tattcttttt ataggttttg gcaaaggttg ataaaaggcc tatggaatta ctgctggttg       480

ctgcacttac atattttgaa tgtcttgaga tgcattgttc tcagtgtatt taattttctt       540

atcttcttta aattctgact cttgacacat actgaaagac cccacctgta ggtttggcaa       600

gctagctgag gatcgtttcg catgattgaa caagatggat tgcacgctgg ttctccggcc       660

gcttgggtgg agaggctatt cggctatgac tgggcacaca gacantcggn tgctctgatg       720

ccgccgtgtt cggctgtcan ncagggcnc ccgntttttt tgnaanaccn nctgnccggg       780

ccctnatgaa ctgnngacaa ggcacccggt ttntnggttg ncnaaanggn gtttnttgc       839
```

<210> 116
<211> 815
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(815)
<223> n is a, g, c, or t

<400> 116

```
tnggggacca gcttgccant tctacaggtg gggtctttca gtatgtgtca agagtcagaa        60

tttaaagaag ataagaaaat taaatacact gagaacaatg catctcaaga cattcaaaat       120

atgtaagtgc agcaaccagc agtaattcca taggcctttt atcaaccttt gccaaaacct       180

ataaaagaa tatctaaaat tgcttttta tgaaagttcc tatttattct tgtttccctt        240

accagagagc ctgctttccc cttactgatg agaacacagg gggtcctggg taaagagtcc       300

ataaaattta aaaggagta tgccttggcc tccatgacc ctcttacttc acaataaggc        360

catctttac ctggtttaga tttgcagact aggtccatta gatacgttgt cattaaatac        420

ctatactata ccctaatatt tgtaatcttg acaggtatta ttttcatttt atagacagat       480

ctaggaaaat tacatgactt atcggaatcc cttcaaatat cacagagcaa agtcatgatt       540

ttaacttgtg tttgncactc tgaaactcac actggaattn tgngggaaat nntatccgnt       600
```

```
canaattccc ccnacatgag cgtnanaccc cgaaaaaaga acaangatnt ttttggaacc    660

nttttttttg gggnnaanng gngnngnaaa aaaaaaccnc cnntncnacg ggggtttgtt    720

ggcgganaan aacnccacct tttttccnaa ggaaangntt tnaaaangcg aanaccaaaa    780

ntgtcntttt gnnnggccgg gttggncccn cttna                              815
```

```
<210>    117
<211>    792
<212>    DNA
<213>    Cercopithecus aethiops


<220>
<221>    misc_feature
<222>    (1)..(792)
<223>    n is a, g, c, or t

<400>    117
ttgggggganc gagcggntaa cattttcaca cagaaattcc cgacctcaag tgatatatcc    60

accttggcct ccaaaagtgc tgggattaca ggcatgagcc accgcgcccg gcccttcat    120

gcagtttctc tcactccttt cagaatcgag gagtctgcta ttccatcgac atctaaccca    180

ctcctctaaa ccagcctgca atcccagctg gagaactaca atccaatcag ggattaaatc    240

taaattcctc ccatctgatc actgggatcc ctacccattc aactcccctc ctcctccaga    300

aatgttacca atcccctaaa gcctccaatc acctgttgag ccaccagcca agcgcttact    360

aatccctgtc tcccaagctc agacactccc tgtaattgat ggacacgcag cattgggagc    420

tttcacattg agctcttact ttgaaacttt gaataagaaa agagctgaaa aaagcagatc    480

tcccaatctc ggtgaaactg tagttaaact ccaagtagaa taccccaata aatggatang    540

aatganaaat ctcatatggg ttatatangc antatttana aattttggaa ttataggnnt    600

anggatncaa acttnnanan tantattcca ttggnntttg gngcncccna ngntaaanaa    660

gttnnccnct canaaggaaa nggggngggt nangggctan nccnnaancc annttttggn    720

ggntnggnnn aaanttttn ggnccaantt naaanaaann tnntnaaaaa aanggnnccn    780

ttttttnaaaa aa                                                       792
```

```
<210>    118
<211>    838
<212>    DNA
<213>    Cercopithecus aethiops


<220>
<221>    misc_feature
<222>    (1)..(838)
<223>    n is a, g, c, or t
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81

<400> 118
gggnaaccga gcggntaaca ttttcacaca gaaantcgga aagtaaagcc aatcttagag   60

gctgcaggag gtttgggggc agtatctgat tcagacgctg gctaacgttt cacgatcgcg   120

ttcccttttt tcttccaact cggtaagtaa aaaggcaaga tgagaaattt acgtgctgaa   180

cttaataaat agttggtgga cgtattgcct ttttttttt ttttttggta agggatgaca   240

catctcgtga ctacagttct tttgaggaat aacttttctg ctagtttcca aatcggcacg   300

tgaccaaagt cttttcatag gattttagcg tcctgataaa aatcaatggg cagaatttga   360

ttgcttttta aaaaatgtgt ttgtcctttg gtctctggca ccattgtaat ggaaaatccc   420

tacattgcct gtactctcag aagctgtcca gtggagcaaa actagagata aagaaacctg   480

gaacgattca gttaggaact tttaagaagc cagcctttag tttttccttt agaagattat   540

gcagttatca tgattgcttc tctagaactt cagtgtgtta tttggattcc taaatctaag   600

acaatgctgn ggaagtctgg ggctttttagn attttngggt ctgctgnaga aaatcctcgt   660

ttatactaca aagtttctnt tttggaactt tnggaattgg gcatttttn nnttattatt   720

ngnatgntng antnannggc aaaactnagn naacccttt nggtttgcct cnanccggtt   780

nttaaanaaa ngggaaaaan cctnanttta aanttttttc caccctttt tntttnt   838

<210> 119
<211> 820
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(820)
<223> n is a, g, c, or t

<400> 119
ttggggganct agcttgccaa ntctacaggt ggggtctttc agtgggggc tgtcctgtag   60

gttatagaat gtttagcagc aaaaattaaa aattaaataa caaaaataaa aataaaaaag   120

aatgtttagc agcatccctg gcctctaccc actagatgtc agcagcacct cccttgcccc   180

caggtgtgaa ccaaaaatgc ctgcagacat tgccaaatat ctcctaggag gacaaaattg   240

tcctctcttc cacttgagaa ctattactct aaaattaccc agatctgctt tgaatccccg   300

ctccaccccca tcacaacctg ggtcatcttg gaaaacagac tgaaccttcc tatgcccccc   360

gcaaattcct caactgtaac atggagctct tgctgaagaa atgctatgaa aattaaatga   420

aatgatgtac gtacaggatt tacacgcaca gaatattcac cgcgccagag tgagtgctca   480

ataaatggtc agaaatgagg ggaggctaaa aaaaaataat ttcgagaact caaaaatctt   540

atctttaggc ctccagagta ctgtagtcta gacagaagaa atggttgaga tagaancaaa   600

agagatgaga gaggttggaa aagaagtgat agaactaagg tattattccc cttatctctt   660

aagaacccgg cttggagtca aagccaatag agggtctact tagttttgnc tattactcta   720

ctttcaaata taacgaaaat tgcccaaacc caaagtntcc aaaaaaaact ttnnnttnan   780

cggggatttc tncncggncn aaaatctaan nccccnctnc   820

<210> 120
<211> 797
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(797)
<223> n is a, g, c, or t

<400> 120
ttggggttgc gagcggntaa cantttcaca cagnaattca gctgatgaat gcagatatga   60

accgatggtt caagagctgt agacatacat acctagttta ccacactgat cttcttagta   120

taaaaaaaca agcgttacta agaaacatct actttcagca aatggacatg accagaatga   180

tacatagaat gatgcaagaa atttcactct accattcatt ttaatcttta cagtaacagg   240

atgattgcta tctcaatctg tcattttacc tttttttttt ttttcagaag ttaaagtgta   300

tccatacaag ttcaacttaa cattgttaag tgcaaagtta acagtgtaca ctttggagat   360

acctttttag gtagaaaatg attttttgtt ttctaataag ttttcccaag taatattaaa   420

gaaggttaaa tatgtcattt acttggagaa aacagaaaac catgagaaag tttgggaaaa   480

tgctatattt cagagcttaa tatattgaaa cagtaagtaa gacaggaatt ggctaccttt   540

taagaacgtt tacaaaaata caaactgann ggaatgcttt tggcaatnaa aatntgacnt   600

gaaacattca atggcnnaac attcaanaan gnttnagana tcnttncctt tancatccaa   660

natngttttg ncgncntctc aaaaaantgt ntntttaaa aaanttaggg ntaaaanttt   720

ctggnagntt nattaanctt tttttgnncc ctnaaatttt nnccnaaagt tcnttnanca   780

aaaaaaaatn ctttttt   797

<210> 121
<211> 828
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(828)

83

<223> n is a, g, c, or t

<400> 121
ttggggancn gcttgccaan tntacaggtg gggtctttca ccttcttgcc agaaacataa   60

aatgcgatgg agctacggcg accgctgccg agacaaaatg gcgccgagaa cctggtttag   120

cgcaggcgcc ttggaaagac cctgccccgc ccccgtgcaa gccctggct gcaattctgg   180

gttccgtttc catgggacac tccgccgcca atcctcgtgc cgaactgctc ttcctgaccc   240

ctcaattcac caatcagtgc ccagtcaagc acatccggag tcgtctctac caatcatttc   300

tcaagacttg cttactcaat aaccaactct ccaataacgt tggtcttcgg aaaaagccaa   360

tcataagtgg aagatgtcct acctgctgtt tttcgcacca atccatgaag tttcagagct   420

acatccaatg aggacggcag gtagcgaggt cctatccgaa gctcttcggc gtcatgaaca   480

gccaatagga gttcgtgtag aagcgagtct gctcaacagc ttgttatttg gtggattgtg   540

gcagtaaatc ggggcgagtg gggaaccggg cgcaggaact gcagccgcgg ttgggagtgg   600

cgcacttnac ccgcanttgg taggtggggg agaggggaat cngggggatn ctgaatggac   720

aaancggnan cggcagcaan tgntgntgcc cgggtncccg tgcaantnga aacntttggn   780

gtggggaang ggattctagg caanggnccc gcnancccna aaaaaggc   828

<210> 122
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(842)
<223> n is a, g, c, or t

<400> 122
ttggggancc tagcttgcca antctacagg tggggtcttt caccttcttg ccagaaacat   60

aaaatgcgat ggagctacgg cgaccgctgc cgagacaaaa tggcgccgag aacctggttt   120

agcgcaggcg ccttggaaag accctgcccc gccccgtgc aagcccctgg ctgcaattct   180

gggttccgtt tccatgggac actccgccgc caatcctcgt gccgaactgc tcttcctgac   240

ccctcaattc accaatcagt gcccagtcaa gcacatccgg agtcgtctct accaatcatt   300

tctcaagact tgcttactca ataaccaact ctccaataac gttggtcttc ggaaaaagcc   360

aatcataagt ggaagatgtc ctacctgctg tttttcgcac caatccatga agtttcagag   420

ctacatccaa tgaggacggc aggtagcgag gtcctatccg aagctcttcg gcgtcatgaa   480

cagccaatag gagttcgtgt agaagcgagt ctgctcaaca gcttgttatt tggtggattg   540

tggcagtaaa tcggggcgag tggggaaccg ggcgcaggaa ctgcagccgc ggttgggagt   600

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ggtgctgccc ggacgggggc cccacggagg tcagagggga ggaggactct ggagctgaca    660

gcgcgcactt cacccgcagt tggtaggtgg gggagagggg aatcgggggn annctgaatg    720

gacaaancgg cacgggnagc aantgntgnt gcccnggggt cccggngcaa ttggaanctt    780

ttggaggtgg gggnanggna ttctagccaa ngggcccnnc nagcccaaaa aaangggncc    840

nc                                                                   842
```

```
<210>  123
<211>  815
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(815)
<223>  n is a, g, c, or t

<400>  123
ttgggnaacc gagcggntaa cnttttcaca cagaaantcc caggctccat gcctgaatag    60

ctgggactac aggcacacag aatcatgccc atctaccttt ttattttttg tagagaagag   120

gtctcactat gatgcccagg ttggtctcaa acacctgtac tcaagagatc ttcccacctt   180

ggcctcccaa agtgccagct ttacaaatgt gagccactgt gggtggccat gaactcttcc   240

aatgaccctt tttcaaaaaa atatttcaac tattcaatgt gagccaagga tgtgccagac   300

atttgctaga tgctatgaat aaaatatgac aaagattcag tctttgtccc catggacttt   360

atagtctagt agtagatgag actcataagt aatatctagc caaaaataaa aattactgta   420

ttatgggaga ataagaatat ggtactaatt tcttcagtgc caatgtatat cttttcatgt   480

tcttgttcct tggattctca caacaattga tgaaaaatgt aacactggat ttgagtttgt   540

agtcttattt tccaacatga tgaagttgtt attaagtgtg agatgatcaa gggagactca   600

ggaagcagtg ggtaacctca gctaaaagca aacagatagt atattggaag atgaggtaaa   660

caaagagagc aaagctttat gaatctgggc taaaantcag ctataagtnt tcgcanatcc   720

angagaactt tncaacagnt tncaattgaa ancctttnag tttttaaann cctnttttn    780

caaantgncn aaannnttaa caggnttgna atncc                             815
```

```
<210>  124
<211>  823
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
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<222>   (1)..(823)
<223>   n is a, g, c, or t

<400>   124
ggnnttgcga gcggntaaca atttcacaca gaattcaaac tccagcttta ctaccctgtg   60

accttgggca ggtcacttca catttctcag gctggtttcc agtctggctg cctttgggga   120
ggggacctgg gtttgcagga agaaaacttc cttacactga ataattattg ccttgttaga   180

aatttttttac catgtgcaca tattactttt cctaaatatt tgcacccaat ttaattgatt   240

taattgggga aaaatgaaca taggaaaaat aatgacctct tcctcagggt tattaaaagg   300

tttcaaaata aagtatgtag ctagtaaagg tgcatagtat atgcttaatc aatagagtgg   360

tgacagggtg gagggaggtg ggaggcaggc tcattcctgc cctggggccc agaggagaac   420

atgtggtaca gaagtcccag cctacagcca gctcctagca ttaaggcagg tgcccattca   480

gctagagcct canggggggtg cnagttgagg gagctgctcc tancctggnc cccatgccct   540

ttnctttgtg gtggancctt aagaagcccn ttttcctgan naanncctgg gnttananaa   600

ttcacctttg ncaattncca agnncccggn gnaattntcc ntnttgggng aaacccnttn   660

nntttaaggg tgnntnttng ggattngnac cnnnnttttg gggcncncc ngnttttttnn   720

tttttnttnn aaannccnnn aaaanaaaaa aaaaanntnn gngnccnnaa annccccnn   780

gggggggaa aaaaaaaaa antttttccc cccccccnc cnc   823

<210>   125
<211>   691
<212>   DNA
<213>   Cercopithecus aethiops

<400>   125
cctaatccac caaccccaa ctactatagt gggagcctga ggtcacagca tggcccccc   60

gtgttgtgag aaaaatctcc acaggattct cccactgttt cctaagtgtg ctctgggatc   120

ctccgtgact agtgtggaat tttgagccag tgatttctcc ccacaggttt caattaaatc   180

atctgtcaaa tgaggatgac cacatcttct ttacctcacc actgagctgt gaaatgaacc   240

agaggcctta ccttttcccc ctgaactccc agtcatccct ggaacaccaa tttgaacatc   300

atctcccact ttcccagcca gttagcagct ctgtcctctg gattttcaaag agaaatgtct   360

ctagcatcat ccctgttttcc ttgcactgtc ctactttctt tttccccccca gagccaggaa   420

tgtcttaaac agaatgagat gctcccaagg ggccaccaac tcacaattag gagttcaata   480

aatactgact taagagtgaa tgaacgatcc ccgtgtcttt gtccacattt gtacatgctt   540

acatgattct gcaaagaatc taaatttctc tttacattaa caaacaaggg ggctgggcat   600

ggtggctcat gactgtaatc tcagcatttt tgttaaccag gacagtcctg atgaaataac   660

tgggaaagtt cctttttggg gggtggggtg g   691

<210> 126
<211> 748
<212> DNA
<213> Cercopithecus aethiops

<400> 126
ccatcgcctt actattgcct tcttgacgag ttcttctgag cgggactctg gggttcgaaa   60

tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata   120

gaaaagttca gatcgaggtc aggaacagat ggaacagggt cgaccggtcg accggtcgac   180

cctagagaac catcagatgt ttccagggtg ccccaaggac ctgaaatgac cctgtgcctt   240

atttgaacta accaatcagt tcgcttctcg cttctgttcg cgcgcttctg ctcccgagc   300

tcaataaaag agcccacaac ccctcactcg gggcgccagt cctccgattg actgagtcgc   360

ccgggtaccc gtgtatccaa taaaccctct tgcagttgca tccgacttgt ggtctcgctg   420

ttccttggga gggtctcctc tgagtgattg actacccgtc agcgggggtc tttcagcagg   480

gcccggggcc acagaaggaa aacatctctg tggaatgtgg aaatgcagaa ctctactggg   540

cccgtttaga aagcacagaa aagcatggaa gaaagggaga ggcgagaagc ctagaaaatt   600

accctagatc ttaggtatgg atatatcgac ctaaaagaaa gaagatgggg caaagttaat   660

gcaagcagag agtttatttg gggtcaagct tgaggattgc accccaggag catagattca   720

agttgccctg aatttacact gattagca   748

<210> 127
<211> 708
<212> DNA
<213> Cercopithecus aethiops

<400> 127
gccaaaccta caggggggt tctttcactg ccagtcagcg aaccgcgaag ccggcaggca   60

cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc   120

ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc   180

actgcgcagc cgtggacacc gccccacgtc gtagggccgt ggaccctgac aacgccggaa   240

cccggcgtcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgcga   300

ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg   360

gcactttcct gtccgcgact ccgcccccgc cagagggct aggctccggg tttcaagatg   420

gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct   480

tacatcacca gcatcgcaga cctcacgggc caggttgctc tgtacacctt ctgccccaag   540

gccaaccagt gggtgagtgc cgcctggctc tgaggacggc cgcccggccg ctgcggtctc   600

ttaaaggggc cgtgcgtgtt gctgtggggt gggggacaca gcaagagcca gggaggtgaa   660

gacggggcca gggactgccg agaagccgac cagaaccaga ggggttgt   708

<210> 128
<211> 741
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(741)
<223> n is a, g, c or t

<400> 128
taacaatttt cacacagaaa ttcaatccaa caaacaanta catattattt tctaagttgt   60

aaagcctgta accgaatgag ttaattagga agggtcaatt acaagaaagt gggaaattat   120

gctagttgtt tttaaacaac taacaaagct tcaagcaggg gctaacgaga atcagtgaac   180

agactgaatg taacttttcg gaccctctcc agtgcacgaa aagccagaaa gtactgagtc   240

tgaggggaac attcagagat gacatcacca gcatcatagg tggaacaaaa cacatttaca   300

gggtctctct tgtttgtaca aaggtcttcg gggatctagt gaacatggaa gcccttttcc   360

taagtgcctt gaaatctttt ccgaaactgt gtagttcgat taaagccgga cccaccgcac   420

tccccttcc aagaatcgaa actaattgga ttttaagctt taaatccaaa tgacctctga   480

gaaagggct ctcatttacg tctgccgggg gagaggagga gtgtttattt tatagacaat   540

gtatatgcaa tttatctaat aatccgcaaa gcctcaaaca caagctttca ggcactcttt   600

tgaccccacc ggtctcataa ctccaatgt atctgcaaag aaggcaggtc gcccacgtcc   660

ccaaacccga cgccaaggga ctgatcctgc tccaatcctc cctcactggc ttttccttgg   720

ggatgtgtnc agcccacttc t   741

<210> 129
<211> 694
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(694)
<223> n is a, g, c or t

<400> 129
ccgccaacct acagggtggg gttctttcac tgccagtaca gcgaatcgcg aagccggcag   60

gcacttcggc ggtctccagc ctttgcctga aaagagctcg gcaagctagc tagaggtcag   120

accccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc   180

```
ttcactgcgc agccgtggac accgccccac gtcgtagggc cgtggaccct gacaacgccg      240
gaacccggcg tccggtgcgt gcgcttggcg gaccagaatg gctaacgtac cgccatgccg      300
cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatggggggaa ccttgcctcg     360
atggcacttt cctgtccgcg actccgcccc cgccagaggg gctaggctcc gggtttcaag      420
atggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac      480
ccttacatca ccagcatcgc agacctcacg gccaggttg ctctgtacac cttctgcccc       540
aaggccaacc agtgggtgag tgccgcctgg ctctgaggac ggccgctccg gccgctgcgg      600
tctcttaaag gggccgtgcg tgttgctgtg gggtggggga cacagcaaga ggccagggga      660
ggtgaagacg gggccaaggg actgncgaaa agcc                                  694
```

```
<210>   130
<211>   678
<212>   DNA
<213>   Cercopithecus aethiops

<400>   130
cccctttactg ccagacagcg aaccgcgaag ccggcaggca cttcggcggt ctccagcctt      60
tgcctgaaaa gagctcggca agctagctag aggtcagacc ccaggaccca gtcgtttag       120
ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc actgcgcagc cgtggacacc      180
gccccacgtc gtagggccgt ggaccctgac aacgccggaa cccggcgtcc ggtgcgtgcg      240
cttggcggac cagaatggct aacgtaccgc catgccgcga ggcccacgta gaggcggaag      300
ttgatgggac ggacgcagat gggggaacct tgcctcgatg cactttcct gtccgcgact       360
ccgcccccgc cagaggggct aggctccggg tttcaagatg gaggcgctga gtcgagctgg      420
gcaggagatg agcctggcgg ccctgaagca acacgaccct tacatcacca gcatcgcaga      480
cctcacgggc caggttgctc tgtacacctt ctgccccaag gccaaccagt gggtgagtgc      540
cgcctggctc tgaggacggc cgcccggccg ctgcggtctc ttaaaggggc cgtgcgtgtt      600
gctgtggggt ggggggacaca gcaagaggcc agggaagttg aagacggggc caagggaact    660
ggccgaaaag ccaagcca                                                    678
```

```
<210>   131
<211>   712
<212>   DNA
<213>   Cercopithecus aethiops

<400>   131
cccgccagcc tacaggtggg gtctttcact gccagtacag cgaaccgcga agccggcagg      60
cacttcggac ggtctccagc ctttgcctga aaagagctcg gcaagctagc tagaggtcag     120
```

```
accccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc    180

ttcactgcgc agccgtggac accgccccac gtcgtcgggc cgtggaccct gacaacgccg    240

gaacccggcg tccggtgcgt gcgcttggcg gaccagaatg gctaacgtac cgccatgccg    300

cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgcctcg    360

atggcacttt cctgtccgcg actccgcccc cgccagaggg gctaggctcc gggtttcaag    420

ttggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac    480

ccttacatca ccagcatcgc agacctcacg ggccaggttg ctctgtacac cttctgcccc    540

aaggccaacc cagtgggtga gtgccgcctg gctctgagga cagccgcccg gccgctgcgg    600

tctcttaaag gggcccgtgc gtgttgctgt ggggggtgggg gaacacagca agaggccagg    660

ggaggtgaag accgggggcca gggacctggc gaaaagcccg aaccagaagc cc            712
```

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<210>  132
<211>  738
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(738)
<223>  n is a, g, c or t

<400>  132
gccagcctac aggggggggt ctntcactgc acagtacagc gaaccgcgaa gccggcaggc    60

acttcggcgg tctccagcct ttgcctgaaa agagctcggc aagctagcta gaggtcagac    120

cccaggaccc agtcgtttta gctcagggaa aggaagcgcc ggacgccagc ctgcaagctt    180

cactgcgcag ccgtggacac cgccccacgt cgtagggccg tggaccctga caacgccgga    240

acccggcgtc cggtgcgtgc gcttggcgga ccagaatggc taacgtaccg ccatgccgcg    300

aggcccacgt agaggcggaa gttgatggga cggacgcaga tgggggaacc ttgcctcgat    360

ggcactttcc tgtccgcgac tccgcccccg ccagaggggc taggctccgg gtttcaagat    420

ggaggcgctg agtcgagctg ggcaggagat gagcctggcg ccctgaagc aacacgaccc     480

ttacatcacc agcatcgcag acctcacggg ccaggttgct ctgtacacct tctgccccaa    540

ggccaaccag tgggtgagtg ccgcctggct ctgaggacgg ccgccggcc gctgcggtct     600

cttaaagggg ccgtgcgtgt ttgctgtggg gtggggggaca cagcaagagg ccagggaggt    660

gaagacnggg gccagggnac tggcgaagag ccgagccaaa gccagagggg tgtcgggtcc    720

acctgggaat tggggggaa                                                  738


<210>  133
<211>  757
```

<212> DNA
<213> Cercopithecus aethiops

<400> 133

```
cgccaaacct acagggggg tctttcactg ccagacagcg aaccgcgaag ccggcaggca        60
cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc       120
ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc       180
actgcgcagc cgtggacacc gccccacgtc gtagggccgt ggaccctgac aacgccggaa       240
cccggcgtcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgcga       300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg       360
gcactttcct gtccgcgact ccgcccccgc cagaggggct aggctccggg tttcaagatg       420
gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct       480
tacatcacca gcatcgcaga cctcacgggc caggttgctc tgtacacctt ctgccccaag       540
gccaaccagt gggtgagtgc cgcctggctc tgaggacggc cgcccggccg ctgcggtctc       600
ttaaaggggc cgtgcgtgtt gctgtggggt ggggacaca gcaagaggcc aggggaggtg        660
aagacggggg ccaggggact ggcgaagagc ccgagccaga gccagagggg tgtcgggtcc       720
acctgggatt gggggggatag gaagtgagaa gaagtgg                               757
```

<210> 134
<211> 668
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(668)
<223> n is a, g, c or t

<400> 134

```
ccagcctaca ggggggggtt ctttcactgc cagtacagcg aaccgcgaag ccggcaggca        60
cttcggcggt ctccagcctt tgcctgaaaa gagctcggca agctagctag aggtcagacc       120
ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg gacgccagcc tgcaagcttc       180
actgcgcagc cgtggacacc gccccacgta gtagggccgt ggaccctgac aacgccggaa       240
cccggcgtcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgtga       300
ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg       360
gcactttcct gtccgcgact ccgcccocgc cagaggggct aggctccggg tttcaagatg       420
gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct       480
tacatcacca gcatcgcaga cctcacgggc caggttgctc tgtacacctt ctgccccaag       540
```

gccaaccagt gggtgagtgc cgcctggctc tgaggacggc ccgcccggcc gctgncggtc   600

ntcttaaaag gggcccganc gtgtttgctg tggggtggg gggacncaag caagaaggcn   660

cagggagg   668

<210> 135
<211> 752
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(752)
<223> n is a, g, c or t

<400> 135
gcttgccaaa cctacagggg gggtctttca ctgccagaca gcgaaccgcg aagccggcag   60

gcacttcggc ggtctccagc ctttgcctga aaagagctcg gcaagctagc tagaggtcag   120

accccaggac ccagtcgttt tagctcaggg aaaggaagcg ccggacgcca gcctgcaagc   180

ttcactgcgc agccgtggac accgccccac gtcgtagggc cgtggaccct gacaacgccg   240

gaacccggcg tccggtgcgt gcgcttggcg gaccagaatg gctaacgtac cgccatgccg   300

cgaggcccac gtagaggcgg aagttgatgg gacggacgca gatgggggaa ccttgcctcg   360

atggcacttt cctgtccgcg actccgcccc cgccagaggg gctaggctcc gggtttcaag   420

atggaggcgc tgagtcgagc tgggcaggag atgagcctgg cggccctgaa gcaacacgac   480

ccttacatca ccagcatcgc agacctcacg ggccaggttg ctctgtacac cttctgcccc   540

aaggccaacc agtgggtgag tgccgcctgg ctctgaggac ggccgcccgg ccgctgcggt   600

ctcttaaagg ggccgtgcgt gttgctgtgg ggtgggggac acagccagga ggccaaggga   660

ggtgaagacn ggggccaggg actggcgaag agccgagcca ganccagagg ggtgtcgggt   720

tcacctggga ttgggggata ggagtgagag aa   752

<210> 136
<211> 739
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(739)
<223> n is a, g, c or t

<400> 136
ctttcactgc cagnacagcg aaccgcgaag ccggcaggca cttcggcggt ctccagcctt   60

tgcctgaaaa gagctcggca agctagctag aggtcagacc ccaggaccca gtcgttttag   120

```
ctcagggaaa ggaagcgccg dacgccagcc tgcaagcttc actgcgcagc cgtggacacc      180

gccccacgtc gtagggccgt ggaccctgac aacgccggaa cccggcgtcc ggtgcgtgcg      240

cttggcggac cagaatggct aacgtaccgc catgccgcga ggcccacgta gaggcggaag      300

ttgatgggac ggacgcagat gggggaacct tgcctcgatg gcactttcct gtccgcgact      360

ccgccccgc cagaggggct aggctccggg tttcaagatg gaggcgctga gtcgagctgg       420

gcaggagatg agcctggcgg ccctgaagca acacgaccct tacatcacca gcatcgcaga      480

cctcacgggc caggttgctc tgtacacctt ctgccccaag gccaaccagt gggtgagtgc      540

cgcctggctc tgaggacggc cgcccggccg ctgcggtctc ttaaagggc cgtgcgtgtt      600

gctgtggggt gggggacaca gcaagaggcc agggaggtga agacggggcc agggactggc      660

gaagagccga gccagagcca gaggggtgtc gggtccacct gggattgggg dataggggtg      720

agagaagngg ctgganaat                                                   739
```

```
<210>   137
<211>   707
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(707)
<223>   n is a, g, c or t

<400>   137
gccaaaccta caggtgggat ctttcactgc cagacagcga accgcgaagc cggcaggcac       60

ttcggcggtc tccagccttt gcctgaaaag agctcggcaa gctagnttag aggtcagacc      120

ccaggaccca gtcgttttag ctcagggaaa ggaagcgccg dacgccagcc tgcaagcttc      180

actgcgcagc cgtggacacc gccccacgtc gtagggccgt ggaccctgac aacgccggaa      240

cccggcgtcc ggtgcgtgcg cttggcggac cagaatggct aacgtaccgc catgccgcga      300

ggcccacgta gaggcggaag ttgatgggac ggacgcagat gggggaacct tgcctcgatg      360

gcactttcct gtccgcgact ccgccccgc cagaggggct aggctccggg tttcaagatg       420

gaggcgctga gtcgagctgg gcaggagatg agcctggcgg ccctgaagca acacgaccct      480

tacatcacca gcatcgcaga cctcacgggc caggttgctc tgtacacctt ctgccccaag      540

gccaaccagt gggtgagtgc cgcctggctc tgaggacggc cgcccggccg ctgcggtctc      600

ttaaagggc cgtgcgtgtt gctgtggggt gggggacaca gcaagaggcc agggaggtga      660

agacggggcc agggactggc gaagagccga gccagagcca gagggggt                    707
```

<210> 138
<211> 818
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(818)
<223> n is a, g, c or t

<400> 138
tcacacagaa ttcagnaaag cacagctgtc taggcgtttg gctcctgaca aatggttgcc   60

tgcccctcac ctcaccagcc tctccagaca cctctgcatc acacagcact gatgaccgcc   120

tcccagccca acacccactc tgcttactct gtgccgccag gctctgattg tgtttgggag   180

gtaaagtgct cagccccaag actggccaaa cttggccctc atcatcccat tcctccttgc   240

cagtggttta tctaggaata gatatggggc cctgttcagg tcagtgaaat gtaagggtga   300

gttagttcag gaatttctga gaaagattct cctctgtaat aaagcagaga gtcacatgac   360

tagaaaatct ttttgttgtt gttgttgttt taccaccacc ccttccttcc tgctttggaa   420

atcggtttat gatgtgatgc ctggagctgt ggcagctgtt ttatgaccat gagagaaggc   480

ttctccagtg tgctaggatt caggggagga aatacagaat gaatgtcagc cctcgatgac   540

actgccgagc cctaaaccaa ctctgagaat ttaagacttt ttgttctgta agaaatgaga   600

tttatttatt gtttaagact ctgttgggta ttctgttatc tgtggcccan aatattttaa   660

ataatataat ttcttttgc aataatacat ctcagatgga cattcccaa agtctaagac   720

tttgagagaa gtcatctctg aagagccaag cattcataat tagaaacttg gccaggtgca   780

gtggctcacg cctgtgatcc cagcactttg ggaggcca   818

<210> 139
<211> 581
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(581)
<223> n is a, g, c or t

<400> 139
cacacaaatt agnncaggtc atcctcctgg tggttcctgt accagtcctc gatcacctcc   60

tcaaactctt ccaccagcac gtcgcactgt taatcgtaac acctcacgtt ggcaaagccc   120

cagcacctta ctcactccta gaggagctca gctaagcctt gcaacccact gcaaggtagt   180

ggcagtggtt cacctaagga aactgaggct agagaggtga aatgacgtga ccaaagccac   240

```
cctggcctgg gtggccctcc tcagagcaga cccaatcccc accggcccct cactgggcac    300

agcaaccctt ccaagggctg aagggcctgt acctgcttct tgaggtcagc cacctctgca    360

gaagtctcgt tccacagctc ataggggatg tccatcacca ccttgacccc tttgtgtacc    420

aggttgtgta atgtctcaaa ggtctctgac atgccctgga agaagcgacc agacatggga    480

ggcagagctc ccttctctcc ctcctaccct cctctcccag tggggcctat gaactcagct    540

gtaagaccaa tgcccaatgc cctctgagga tcctcaaacc t                        581
```

```
<210>   140
<211>   630
<212>   DNA
<213>   Cercopithecus aethiops

<400>   140
tcacacagaa ttccatgttc agtaaccagg tgctacaaat gcagttcaag gctctaggtc    60

atgacaatgt cacagatatc tcaggtccag tcaccaaggc aacatgtggc ttgggtcttt   120

ttctggtttc aagactgcat ctgtattctc tcacctccct gggcccacag attccctaaa   180

tcatagcttg gtctaagagc aatgcttcaa attcaggtcc cttgtctcag gtgggtagac   240

ttcctgtcac ccagccaccg ccacctgatt ctggacctgg agccggcagg ccgtggctt    300

cagcccgact cactcttttg tattctgttg cttactatca tctttttttt ttttggtctt   360

gaactccgca gtgtcatttt ttttttctag tttatccatc tttgccatgt gtttggggaa   420

gaatggcaat gcgaaagtgt gaacttccag tcccggctta ttagaagccc acagctgttt   480

taaaaaaaat ctaccttgct atcctttccc tttctgtga cacacaagtg actgttaatt    540

agtacctagg ccatgggctg tcatgcttaa aaactgaatg gaatttttg ttctttagc    600

aatgttagga tgactggctg attataaaaa                                    630
```

```
<210>   141
<211>   737
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(737)
<223>   n is a, g, c or t

<400>   141
acacagaatt cttacttaat acatataaac agaacatttc taggtcagtg aacaaaaata    60

taacctgaat cataaaaaca gagttataac tcctccatca atttccagac atcagccagt   120

ttacaaatcc agaacccctt aaatgaagaa caagcttgat gcccttgagg aagggcccta   180

gtacactgcc caaaatctgt acatttaatt ttcctcctaa tcttcccaaa agggacatat   240
```

gtcctttac cagtgaaact gctcatttgg gtaattgaaa ataatcaaat caggtactac   300

tggaccctgg ctacgaactg atgcaaattc caggagacct aacatgccat ggtggtccac   360

aaagacagtg cttatgggaa tcaggtgatc catggagttt taagttgggt ccaactcaca   420

tttgaataaa tatactcatg ctgacagaat ctccataatg gttccctgac ctgtaaagtg   540

aggtgcatta tggtgggtaa tggcaaatgg aagccagtag aaacacctct atctaggaaa   600

aatagtaaag caaatgcaat attttcatct ccgtagggat tgcagacatt agttgccacc   660

atcaagggct tgaaaaatga ccaggggggtg attcccacca acattctnca ttcagctttg   720

tctattnggg ccttgcc   737

<210>   142
<211>   768
<212>   DNA
<213>   Cercopithecus aethiops

<400>   142
tttcacacag aattcagtgg atgctatgaa acatatcttc actgttcgtg tttgtctctt   60

tctgaatcca caagtgatgg acacatgaat ctactactac tgttctcttt tcttcttttt   120

ccgtctttct ctcccttccc accctagtt cctgacgttt gcctactcta tcatgtctgc   180

agtgttgcat accactctgc atcctcatct gtctgagaca cattcaacca ctaggtcctc   300

agctgcttca ctgctgcctg atgttctttg aagtccagta taagagagaa cattctattt   360

tgctaaaact aaaagactac cctttatctt tgctgagaat atgtaaagaa aaggggaatg   420

actagatcag aaggcttatt ctgaggtata tagtaatgtt aatttttaaa taattgttag   480

gtgttcttct tcattaggta ttcaccttca gttttccaag actatggaaa gcaccattgg   540

tgcatgtagt taacagcagc ttgactcaga cgtagaactg cagccaggac ccatctgttc   600

cccattactc cctgctgcca gttttgcaac cagaacctag gagtgattta tcccatcctc   660

aattttgctc aggactcagc agaagaagga tcctgggaca caagactttt cagtggcttc   720

aaacttggga gagttctttg gcaatgcaca ggtttgacct atgaactg   768

<210>   143
<211>   450
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(450)
<223>   n is a, g, c or t

96

<400> 143

```
gcctgtgaaa ccatctggnc ctggactttt tttggttggn aggctatcaa cttattgcct      60

caatttcaga gcctactatt ggtctattca gggatctcaa ctncttcctg gctttagtct     120

tggaagagtg taagtgtcca ggaaatctat ccatcttctt ctagattttc cagtttattn     180

cgcgcagagg cgttcacagc agcctctgat ggtagttcga atttctgagg ggncggcggn     240

gatatcccct ttatcattnt naatngcgnc gatnagacnc ttctctcttn tcttctttat     300

aagcactcng ctagccggcc ngccaatntc gnngangctt ntcaaaaaac caactcctgg     360

attcatcgat tncnntggag ggtctntttg ngtctctatc tccttcagtn actgcnctga     420

tcttagnata tttcntgccn tctgctagct                                     450
```

<210> 144
<211> 729
<212> DNA
<213> Cercopithecus aethiops

<221> misc_feature
<222> (1)..(729)
<223> n is a, g, c or t

<400> 144

```
cacacagaat tacccttttc gccttccaag gggaaaccag gccactttgc tcttcttggg      60

gaaggaggat aattgtccag tgctgggagg tgacagcagc tactgccagc acgaggtggg     120

gcccctgcag tgtggttcct caggtctgag aggggttccc tctgccttcc tccctcctgc     180

tccccttttcc tctttcctct acctgttttt tccttctctc acatctctcc tgcttcccca     240

caatccctga catttactgc aggctcccga agagccatga cactttatac cctcaacctc     300

atttaattct caggaaaccc cacaaggccg tgcaattctc accccaggta ccaagtgagc     360

cagttcaggt gcacagagac tgccccttgc ccagagatcc tagcacgagg gctctgtact     420

ggttagggtc tccagagaaa cagctccaat agaatgtgca gatgctgggt gcagtggctc     480

acccctgtaa tcccagcact ttgggaggcc gaggcgggcg gatcatgagg tcaggagatc     540

gagaccatcc tggctaacac ggtgaaaccc catctctact aaaaatacaa aaacattagc     600

cgggccgtgg tggcgggncg cctgtagtcc cagctacttg ggaggctgag gcaggagaa     660

tggcatgaag ccganaggca nagcttgcag tgagccaaga tcacatggca ctccaacctg     720

ggcgacaaa                                                             729
```

<210> 145
<211> 755
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(755)
<223> n is a, g, c or t

<400> 145
aacaattttc acacagaatt acctggtctc aaagtgtatc ctccatgctt cggcctccca   60

aagtattgtg attacaggag tgacccaccc tgcccggccc tctagcttat ggtggaagct   120

taaataatca gttttagaca tttcttcttc ctttttttcc caagaaacag ggtcttgctc   180

tgccacccac gctggaatga agtggtgcaa tcatagctga ttgcaacctc aaactcctta   240

actcaatcaa tcctcccacc tcagcctttc aaatagctgg gactacagtg cgtaagccac   300

cgcacctggc ctcttctttc taatataagt atttaatatt ataaaatttc ctctaagatc   360

taaacactgc tttagctgca actcacaaat tttgatatgt tgtatttta tttatatccc   420

attaaaaata cagtattagt tcccgtgtga tttcttcttt gacccatggc ttagaagtgt   480

gttgtttagt ttccaaattt gggggcattt tccagatatc tttctcttat ttatttgtaa   540

tttaattctg ttgtggtcga ggagcacgtt ctgtttgctt acaatcctcg taaatttatt   600

atgacttgtt ttatggccca gcatagggtc tgtttggcga gtgttccatg tgcatctgaa   660

aagaatgtgt attctgtagt tgtgcagggt atttttaaaa ttttattctt ttcactgana   720

caaaatagct gtncatattt agagggtaca tgcga   755

<210> 146
<211> 795
<212> DNA
<213> Cercopithecus aethiops

<400> 146
ctaccagtat atacaaagaa aagctcgtac cattcatgct gaaactactc caaaaagttg   60

aggagaagga aatcctccct agcttattct acaaagctag catcacactg ctaccaaaac   120

ctgacagagt cacaacaaca aaaattcag acatatattc ttgatgaaca ttgatgcaaa   180

gtagtcaaca aaatacttgc aaaccaaatt cagcagcaca tcaaaaagct tatccatcat   240

gatcaagtag gctttatccc tgggatgcaa ggttggttca acatctgcaa atcaataaat   300

gtgattcatc acataaatac cactaaagac aaaaaaacca catgattatc tcaacagatg   360

cagaaaggc ttttgataaa atccaatacc ccttcatgtt aaaaactctc aataaactag   420

gtattgaagg aacatacctc aaagtaataa gaaccaccta taaaaaaccc acagccaaca   480

tcatattgaa tgggcaaaag ctggaagcaa tccccttgaa aactggagga agacaagaat   540

accctttctt accactccta ttcaacataa tattggaagt cctggccagg acaagcaggc   600

aagagaaaga aagaaaggca tcccaatagg aagaaaggga agtcaaacta tccctgtttg   660

cagacaaaat gatcctatag ctagaaaccc catagtctca gcccaaagct tttaagctga   720

taaacacttt cagcaagcct cagcatacaa aatcatgtgc aaaagtcagt acattttgta   780

caccaccaac agtca   795

<210> 147
<211> 704
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(704)
<223> n is a, g, c or t

<400> 147
gcatcctccc tcctcggcct gggcgtgggc tcgcaaaacg ctgggattcc cggtattaca   60

ggcgggcgcg ccacgccagg agcaaacact tcctgcttta aaaattcagt gttgtgattg   120

gctgccattc agcattatgc taattaagca tgcctgtttt ttttaagctt cttaaaacaa   180

ttttttaaaa ttccgtttcc acctaaaacg ttaaaatttg tcaagtgata atattcgaga   240

agatgttgtt gccaaactat ttttctattt gtttcctaat ggcatcggaa atagcgaaag   300

tatctcgcca ttagttaaaa gttggcagca gatgtagacc ccgcagaggc tgcgagtggg   360

ctgttaagac tatactttca gggatcattt ctatagtttg ttactagaga agttctctct   420

gaacgtgtag agcaccgaaa accacgagga agagacgtag cgttttctcc tgagcgtgaa   480

gcgggcgttt ggtgttgctt cgctgcaact gccatcagcc attgatgatc gttcttctct   540

ccgctttgga gagnaagagg gagagaacgc ggtctgagtg gttttctttt tttgcgnggt   600

tagaacgaca gactgtacag cgaccgtntc ccggcttgnc tntgtgcttg nntgnccncc   660

ngaggccnaa gngagttgcc ttattttgtt tcacnanccg ntgt   704

<210> 148
<211> 650
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(650)
<223> n is a, g, c or t

<400> 148
atcgccttct atcgccttct tgacgagttc ttctgagcgg gactctgggg ttcgaaatga   60

gctagccctt aagtaacgcc attttgcaag gcatggaaaa atacataact gagaatagaa   120

99

aagttcagat cgaggtcagg aacagatgga acagggttga ccggtcgacc ggtcgaccct   180

agagaaccat cagatgtttc cagggtgccc caaggacctg aaatgaccct gtgccttatt   240

tgaactaacc aatcagttcg cttctcgctt ctgttcgcgc gcttctgctc cccgagctca   300

ataaaagagc ccacaacccc tcactcgggg cgccagtcct ccgattgact gagtcgcccg   360

ggtacccgtg tatccaataa accctcttgc agttgcatcc gacttgtggt ctcgctgttc   420

cttgggaggg tctcctctga gtgattgact acccgtcagc gggggtcttt cagttaagac   480

tatactttca gggatcattt ctatagtttg ttactagaga agtttctctg aacgtgtaga   540

gcaccgaaaa ccacgaggaa gagacgtagc gttttctcct gagcgtgaag cgggcgtttg   600

gtgttgcttc gctgcactgc catcanccat tgatgatcgt tttntntccg   650

<210>   149
<211>   671
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(671)
<223>   n is a, g, c or t

<400>   149
aactttaact aatggcgaga taccttcgct attgccgatg ccattaggaa acaaatagaa   60

aaatagtctg gcaacaacat cttctcgaat attatcactc gacaaattat aacgttttag   120

gtggaaacgg aactttaaaa aattgtttta agaagcggaa aaaaaacagg catgcataat   180

tagcataatg ctgaatggca gccaatcaca aactgaatct ccaaagcagg aagtgtttgc   240

tcctggcgtg gcgcgcccgc ctgtaatccg ggaatcccag cgtttagcga gcccacgccc   300

aggccgagga gggaggatcc tttgttccac gagatcgaca ccagcctagg caatatagca   360

gaatcctggt ggtgacggaa atgccctatc ttgagcttat caatgccaaa accccggtca   420

tataacttta ttggatatca gtggggaaaa ctgagtaaaa ggtgcaaatg tataactcag   480

tataaacccc aagaacgaaa cgcaaaacct accattctct gaaagaaatg ttttgtacat   540

atatttacac agaaacacat acatcatgat caaaaaatga catcattcgt aaaaaaaaat   600

aacaaaaagt gtaaaagaac ccatcgcccg gaaaggaagg gccctgtgag accggatccc   660

caaaaccaaa c   671

<210>   150
<211>   704
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(704)
<223> n is a, g, c or t

<400> 150
tcattaacag cccactcgca gcctctgcgg ggtctacatc tgctgccaac ttttaactaa   60

tggcgagata ctttcgctat ttccgatgcc attaggaaac aaatagaaaa atagtttggc   120

aacaacatct tctcgaatat tatcacttga caaattttaa cgttttaggt ggaaacggaa   180

ttttaaaaaa ttgttttaag aagcttaaaa aaaacaggca tgcttaatta gcataatgct   240

gaatggcagc caatcacaaa ctgaattttt aaagcaggaa gtgtttgctc ctggcgtggc   300

gcgcccgcct gtaatccggg aatcccagcg ttttgcgagc ccacgcccag gccgaggagg   360

gaggatcctt tgttccacga gttcgacacc agcctaggca atatagcaga attctgtgtg   420

aaattgttat ccgctcacaa ttccacacaa catgagcgtc agacccgaa gaaaagatca   480

aaggatcttc ttgagatcct ttttttctgc gcgtaatctg ctgcttgcaa acaaaaaaac   540

caccgctacc agcggtggtt tgtttgccgg atcaagagct accaactctt tttccgaagg   600

taactggctt cagcagagcg cagataccaa atactgtcct tctagtgtag ccgtagttag   660

gcccnccact tcaagaactc tgtagcaccg cctacatacc tcga   704

<210> 151
<211> 705
<212> DNA
<213> Cercopithecus aethiops

<400> 151
gctatattgc ctaggctggt gtcgaactcg tggtaacaaa ggatcctccc tcctcggcct   60

gggcgtgggc tcgcaaaacg ctgggattcc cggattacag gcgggcgcgc cacgccagga   120

gcaaacactt cctgctttaa aaattcagtt tgtgattggc tgccattcag cattatgcta   180

attaagcatg cctgtttttt ttaagcttct taaaacaatt ttttaaaatt ccgtttccac   240

ctaaacgtt aaaatttgtc aagtgataat attcgagaag atgttgttgc caaactattt   300

ttctatttgt ttcctaatgg catcggaaat agcgaaagta tctcgccatt agttaaaagt   360

tggcagcaga tgtagacccc gcagaggctg cgagtgggct gttaatgaaa gaccccacct   420

gtaggtttgg caagctagct gaggatcgtt tcgcatgatt gaacaagatg gattgcacgc   480

tggttctccg gccgcttggg tggagaggct attcggctat gactgggcac aacagacaat   540

cggctgctct gatgccgccg tgttccggct gtcagcgcag gggcgcccgg ttctttttgt   600

caagaccgac ctgtccggtg ccctgaatga actgcaggac gaggcagcgc ggctatcgtg   660

gctggccacg acgggcgttc cttgcgcacc tgtgctcgac gttgt   705

<210> 152
<211> 673
<212> DNA
<213> Cercopithecus aethiops

<400> 152
tttcattaac agcccactcg cagcctctgc ggggtctaca tctgctgcca acttttaact   60

aatggcgaga tactttcgct atttccgatg ccattaggaa acaaatagaa aaatagtttg   120

gcaacaacat cttctcgaat attatcactt gacaaatttt aacgttttag gtggaaacgg   180

aattttaaaa aattgtttta agaagcttaa aaaaaacagg catgcttaat tagcataatg   240

ctgaatggca gccaatcaca aactgaattt ttaaagcagg aagtgtttgc tcctggcgtg   300

gcgcgcccgc ctgtaatccg ggaatcccag cgttttgcga gcccacgccc aggccgagga   360

 gggaggatcc tttgttccac gagttcgaca ccagcctagg caatatagca gaattcatct   420

cacagagtta catctttccc ttcaagaagc ctttcgctaa ggctgttctt gtggaattgg   480

caaagggata tttggaagcc catagagggc tatggtgaaa aaggaaatat cttccgttca   540

aaactggaaa gaagctttct gagaaactgc tctgtgttcc tctgaattct ggaagaaaac   600

aaacacatca ttcttgtctc caagagctta aatttctgtt tgggcaattt atttataaaa   660

acacaactta gcc   673

<210> 153
<211> 709
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(709)
<223> n is a, g, c or t

<400> 153
tttcattaac agcccactcg cagcctctgc ggggtctaca tctgctgcca acttttaact   60

aatggcgaga tactttcgct atttccgatg ccattaggaa acaaatagaa aaatagtttg   120

gcaacaacat cttctcgaat attatcactt gacaaatttt aacgttttag gtggaaacgg   180

aattntaaaa aaagtttta agaagcttaa aaaaaacagg catgcttaat tagcataatg   240

ctgaatggca gccaatcaca aactgaattt ttaaagcagg aagtgtttgc tcctggcgtg   300

gcgcgcccgc ctgtaatccg ggaatcccag cgttttgcga gccacgccc aggccgagga   360

gggaggatcc tttgttccac gagttcgaca ccagcctagg caatatagca gaattctgtg   420

tgaaattgtt atccgctcac aattccacac aacatgagcg tcagaccccg aagaaaagat   480

caaaggatct tcttgagatc cttttttttc tgcgcgtaat ctgctgcttg caaaacaaaa   540

aaaccaccgc taccagcggt ggtttgtttg cncgggatca agagtctacc aacctctttt   600

ttacgaaagg tnactgggct tcaggcagga gccgcanatt nccaaaataa ttggnccctt   660

ccaagnggnn ancccgcnag gnttagggcc cnoccaactt tcnaaggac   709

<210> 154
<211> 574
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(574)
<223> n is a, g, c or t

<400> 154
cctcggcctg ggcgtgggct cgcaaaacgc tgggattccc ggattacagg cgggcgcgcc   60

acgccaggag caaacacttc ctgctttaaa aattcagttt gtgattggct gccattcagc   120

attatgctaa tnaagcatgc ctgttttttt taagcttctt aaaacaattt tttaaaattc   180

cgttaccacc taaaacgtta aaatttgtca agtgataata ttcgagaaga tgttgttgcc   240

aaactatttt tctatttgnt tcctaatggc atcggaaata gcgaaagtat ctcgccatta   300

gttaaaagtt ggcagcagat gtagaccccg cagaggctgc gagtgggctg ttaatgaaag   360

accccacctg taggtttggc aagcatagct gaggatcgtt tcgcatgntt gaacaagatg   420

gattgcacgc tggntctccg gccgctngng tggagaggct attcggntat gactgggcac   480

aacagacaaa tcgggctgnt ctgatgccgc cgtgttccgg ntgtaagcgc aggggcgccc   540

cngtttcttt tttgnaaaga ccganctgta acgg   574

<210> 155
<211> 794
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(794)
<223> n is a, g, c or t

<400> 155
actccggaga tatgaggcct agctccatcc ttcttttctt atcactcagt cattcaatct   60

ttgcttggaa tacatgaact aataatttcc aatattacct gacatggatc cactttaggg   120

aagacacaag atatgaaaga aaggataaag tctgaaagtt agaagtaaca caactacaga   180

```
aaatagatta atgtggattg ttatagccat tcatacaatg acatcctcaa cgtcaaaacc      240
tttttgtact ctttacagat tccacatcca agcagaattc tatttaatgt gctttctaac      300

aatcagattc ctgacaaatg tgttcataaa gtaataaaag cagcaaaatc ttaaatgttt      360

tatactaaca tagtagacaa aatacaaata ctctgaacac taatatcaca gaaaccctta      420

aaaaaaagat tgaggggagg taataacata cctaatacaa atagaaataa ggaggaacct      480

ttgaggtttg ctatgctttg aacgtgtccc caaggttcac atgttggaaa cttaatccct      540

gaagcaacag tgatgagaag tgggaccttt aagaggtgag taggtcacga gggctctgct      600

ctgccacatg aatggattaa tgctattacc agaggagtgg ggaatgggtt ccagatagaa      660

gaccgagttt ggcctcctcc ttatntntcg ctctctngcc ttccgccttc taccatggga      720

tgatacagca ggaagaccct agataccaca ccttgatatg gacttccngt cccnanacct      780

tgantaaata ccag                                                        794
```

<210> 156
<211> 831
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(831)
<223> n is a, g, c or t

<400> 156
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cgcatcgcct tctatcgcct tcttgacgag ttcttctgag cgggactctg gggttcgaaa       60

tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata      120

gaaaagttca gatcgaggtc aggaacagat ggaacagggt cgaccggtcg accggtcgac      180

cctagagaac catcatatgt ttccagggtg ccccaaggac ctgaaatgac cctgtgcctt      240

atttgaacta accaatcagt tcgcttctcg cttctgttcg cgcgcttctg ctccccgagc      300

tcaataaaag agcccacaac ccctcactcg gggcgccagt cctccgattg actgagtcgc      360

ccgggtaccc gtgtatccaa taaaccctct tgcagttgca tccgacttgt ggtctcgctg      420

ttccttggga gggtctcctc tgagtgattg actacccgtc agcgggggtc tttcaaggtc      480

aactgacttt aaacttgccg tttgatttgt gactttagaa agtagagtta actatattta      540

gcaatatgct taagcatgtg catatcacct catgaaacgt gtgtgtgcat gagaaaagct      600

gcctccagta catatacata tgtatataaa cacacataca cacaagcata tatatgtatg      660

tatttcttgn aggaccagtc tcattgtata taatttcaag tgcaggttcc tgatctccan      720

ggatgcgtaa aagactcact gaagttngga agaaanttta nggctactat tntgttggng      780

atcncaccct tcaagtttaa atttgatntg attattctta cngnttgcng g              831
```

<210> 157
<211> 637
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(637)
<223> n is a, g, c or t

<400> 157
caacctaaga aaaacttcaca gccactttta aagcagtaac acatgtataa agtatagttt   60

ggatcctttt gtacacagct cctgaaagag agaaattttt ttttcaccta ccgacagaca   120

tattggaagg ctgctaatat tctgactttt acggactgta ctccctttaa cctgggtaca   180

taccataata ttctttcagt tgnccacagc tatagatacc cctagcataa cacttcagga   240

ttcagaagac gaatgtacct ttctgtatct taacctctct actccacact tcccacctct   300

gaaaaaacaa caggccaaat tctcagaacc taaaaccaag tcagagtaaa cactgctaat   360

acaatactga cacttacata tttacctggc ataatctcta ggattccacc cacaacctaa   420

cagatcctaa ctctctcata gagngagaaa atctgctaaa atctgacaga agtccaaatg   480

aatcctttca gatatatgta gcttgctaca cactcagaaa gnnaagttct cggaacttga   540

aagctctctg aaactnttac cagntacaag angttncagc nnatcacact agcagcatgg   600

ntaanggcaa accagagcag ctaccggaan attaaag.   637

<210> 158
<211> 656
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(656)
<223> n is a, g, c or t

<400> 158
tccatacctt taaaattcaa gaatgttgtg ttctaatggc agtttgaccg ttgagatatt   60

aacataggaa catcatttag cctcttaagc ttgaacatcc attaagcggg aaaaatagtg   120

cttatttcct agaggtttgc agacattggc taaccaatag ttntgattnt gctggaaagc   180

aatgtgcaaa ttttcttaga tgtgatcgct tcattttctc ttacatttta gattggcagc   240

agccaaatgg gcgttccagc ccctnatctc ctgcaagatt cttctcagtt tcataaatct   300

ggtaattttt gagctctttt cccaacaggg tgctgcagct caccaagtgg aatctacaac   360

```
attttctgct accaggatag cagcttgcca gcaggatata ctgaaattac tgggtttcag      420

tatgatgttg gctggtacga acntcaatca tncgaatcga catgcgccca gccattctca      480

taatgaaatg tntccttctc ctttcaacat gttccgcttt ccagcccccc atcctccntt      540

tattatnttt tttctttcan nnaaaagaag ctttnagnaa acacnnaaac ctcttactcc      600

ctntagngaa aggaaaacnt tctttccnnt nctncntccc ctttngannc ncccta         656
```

<210> 159
<211> 654
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(654)
<223> n is a, g, c or t

<400> 159
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cattttaatt tttatatagg atggtattta tgaacatccc actaactatt ctgccgctga       60

ttgatatttg gatgtgtaca gtttgatgct attataaaat tcttctaaga acattcttgt      120

acatgttcat tttgtttcgc taggtcctag agtctaaggt atatatccag aagaggaata      180

gctgggtatt atgatagaat aatgacaaac tagtttctaa agtgattgta ccaattagtg      240

tttccatagg agaaaagtgt acagctactg gaaaaacagt ttggaatgat ctgaagtata      300

agaatgttca tagcaacaga atgtgtttct tgtattccaa atgttcacct acagttggtg      360

tggtcagtat aagttgttgt ttttgttttt attgtgtgtg tgtttttttt atcctttggg      420

acagggcctc actttgttat ccaggctaga gagcagtggt acaaacatga ctcactgcag      480

ccttagcctc ccaggctcaa gcagtcctcc tgcctcagcc tcctaagtac ctgggactac      540

aggcatgtgc caccacacct ggctaatttt tgtattttnt tgtagagaca gggtttcacc      600

atgttngccc agtctggtct agttttaaac aaagttgtng cctgnggaaa tgat          654
```

<210> 160
<211> 683
<212> DNA
<213> Cercopithecus aethiops

<400> 160
```
ttactgcatc tgcacacaaa aacccaccga agaaaaaaag tgtgaatgcc atacaatttt       60

tttcaatgca agtatggaac actgtacatc actgaaaaac aggggggaaaa aaaaaaagga     120

aaaagaggag aaccattgaa gaaagcataa aatagcagct agctttctta cgtgtgctgg      180

aattgtgtct ttcgggttaa ccccaaattt tcctatgcta tacactcttc tcacattttg      240

gtcaatacta gcttctgaat tggaagaggc attatcaatt gctttaaaat gttataccta      300
```

```
aaataaagaa acactgagtt agactgtcac cactttgaat acccatcagg agagtgtggc        360

attgcatgcg aaaatgtatg tgttcctctt aggagatgaa gatcaagtca gctaacagct        420

gtcaacaaac ttctagtgta ggcaagaatt ttatggccaa gttgggcttt cctttattcc        480

ttactggaag aaagtattca gaaaatagca ttttagggga aaaaagtgtt aagtaaacag        540

aatcctttta agcacacaaa caaaagttga gcagtgtaaa ttttgaaact tagtgccttt        600

tagtatctga agcaaaatga taacaagtta taggattttt tctttatgaa gaatgatgta        660

agctcactta tgaaagaaga acc                                               683
```

```
<210>   161
<211>   811
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(811)
<223>   n is a, g, c or t

<400>   161
ctttcacgag aattctgtct caaaaaaaaa aaaaagcca aagtcctcaa aatggcctgc        60

atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt        120

tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg        180

gatctgaaag gctcacaccc tcacctcctt cagaggtttg ctaaaatgtc ttctacccag        240

tgaagccttc cccaaccacc acattaaaaa cacacaacca gcacccgttc tctatcttcc        300

ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt        360

aattcatact gcaaaacaac ttagtttnta ccatgtgcca ggcattgtcc ctagttgctg        420

acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac        480

attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa        540

agaaaaaaaa gaggaaaggg ctgatttttg tgtctttccc tccanaatgc aagctccctt        600

gaggatacag atttgngtgt tttttaacta ctgnaatnct ccctgacaat agcgccccag        660

tnacatagta agggcatttc gannccaatt ttttaaaaat gaagaaaact aggccagtta        720

ccncagtttc ctggggccca attttcaact ttttagganc ntnaantacc gatataaana        780

aaattcggtt acagctaggg ctccgnatna a                                      811
```

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<210>   162
<211>   757
<212>   DNA
<213>   Cercopithecus aethiops
```

<220>
<221> misc_feature
<222> (1)..(757)
<223> n is a, g, c or t

<400> 162
ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc   60

atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt   120

tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg   180

gatctgaaag gctcacaccc tcacctcctt cagaggtttg ctaaaatgtc ttctacccag   240

tgaagccttc cccaaccacc acattaaaaa cacacaacca gcacccgttc tctatcttcc   300

ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt   '360

aattcatact gcaaaacaac ttagttttta ccatgtgcca ggcattgtcc ctagttgctg   420

acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac   480

attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa   540

agaaaaaaaa gaggaaaggg ctgatttttg tgtcttccct ccagaatgca agctccttga   600

taggcattcg atccaatttt aaaatgagat actaggcagt tactcagttt tctgggcaca   720

tttcaacttt tagacaataa taccgataag aaaanta   757

<210> 163
<211> 749
<212> DNA
<213> Cercopithecus aethiops

<220>
<222> (1)..(749)
<223> n is a, g, c or t

<400> 163
ctttcacgag aattctgtct caaaaaaaaa aaaaaagcca aagtcctcaa aatggcctgc   60

atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt   120

tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg   180

gatctgaaag gctcacaccc tcacctcctt cagaggtttg ctaaaatgtc ttctacccag   240

tgaagccttc cccaaccacc acattaaaaa cacacaacca gcacccgttc tctatcttcc   300

ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt   360

aattcatact gcaaaacaac ttagttttta ccatgtgcca ggcattgtcc ctagttgctg   420

acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac   480

```
attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa      540

agaaaaaaaa gaggaaaggg ctgatttttg tgtcttccct ccagaatgca agctccttga      600

ggatacagat ttgggtgttt tntactactg natctcctga acaatagcgc cccagtacnt      660

aggtaggnca ttcgatccaa nttttnaaaa agaggancct agggccagtt aactnaagtt      720

ttctggggcc ccatttccaa acttttaga                                        749
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<210>   164
<211>   741
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(741)
<223>   n is a, g, c or t

<400>   164
ctttcacgag attctgtctc aaaaaaaaaa aaaaagccaa agtcctcaaa atggcctgca       60

tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt      120

gctcctcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg      180

atctgaaagg ctcacaccct cacctccttc agaggtttgc taaaatgtct tctacccagt      240

gaagccttcc ccaaccacca cattaaaaac acacaaccag cacccgttct ctatcttcct      300

tcactttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta      360

attcatactg caaaacaact tagttttac catgtgccag gcattgtccc tagttgctga       420

caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca      480

ttgggagtga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa      540

gaaaaaaaaa gaggaaaggg ctgatttttg tgtcttccct nccagaatgc aagctccttg      600

aggatacaga attngtgtgt tttttnacta ctgnatctcc tgacaatagc ncccagtaca      660

tagtaggcat tcgatccaat tttnaaaaga ganactaggc angtactaag tttntgggcc      720

cattnnactt ttaagacaat a                                                741
```

```
<210>   165
<211>   727
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(727)
<223>   n is a, g, c or t
```

<400> 165

```
ctacgataca tgtaacattc tacgaacaac catggtgagt agaaccatct ggattttcca     60
tcactttcat ttaaaagact ctgttgatat tctaggtact gattccatat atcagtatca    120
acaaatttct caaccaaggg gataattggt ttatctgttt gcaattcatt ccgtaattta    180
gaaaggagag aaatagcttt cttttcagct tccacgcctt cctgcaaaaa tacaagaaaa    240
atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcg tgtctatgca attcctctag    300
ggtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaactac attatacttc    360
tttaaacatt acatttagaa ctcttaaact gaaaatcaaa aaacacacac agatctcata    420
tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt    480
actacagagg gaaaggaacc cctgacagat tttccatgtc tttcatgctt ccatacacat    540
tcttctttca ccattgacac cactagaaaa gaaactgtgg cctttctgag gtttctttttg   600
gtagctcaat ttttttttttt aacttgtttt ccactgagtt ctagctaggt gagagatgag   660
atatgctgac atacaaggcg ctacaatata tctcacatga caggccantg ggagtgggga    720
naaatgt                                                              727
```

<210> 166
<211> 713
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(713)
<223> n is a, g, c or t

<400> 166
```
cacgagaatt ctgtctcaaa aaaaaaaaaa aagccaaagg tcctctaaaa tggcctgcat     60
ggcactacat tctctggccc tttatcagca ctctgacagc tctctccttt gcttattttg    120
ctcctcattc tagcctctgg atctttgccc ttgctgttcc ttacgctctt ctcccaggga    180
tctgaaaggc tcacaccctc acctccttca gaggtttgct aaaatgtctt ctacccagtg    240
aagccttccc caaccaccac attaaaaaca cacaaccagc accgttctc tatcttcctt     300
cactttgcat ttgtccattg tgtaacatca cttacatacc tttaattttt agtttattaa    360
ttcatactgc aaaacaactt agttttacc atgtgccagg cattgtccct agttgctgac     420
aatacagttg aaaataaaat agacaaaaat cccatctttt gaatcttttg aaccttacat    480
tgggagtgac aggcaaaaac gaggtaaaat cagtaaaata cgtgagacag aacgctaaaa    540
gaaaaaaaag aggaaagggc tgattttgt gtcttcccct ccagaatgca agctcccttg    600
aggatacaga tttnggntgt ttttttacta ctgtatctcc tgacaanagg cgcccagtaa    660
```

```
cataggtang gcattcgatn ccaattttn aaaatgagan actaggcagt tac          713
```

```
<210>   167
<211>   714
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(714)
<223>   n is a, g, c or t

<400>   167
ctttcacgag aattctgtct caaaaaaaaa aaaaagcca aagtcctcaa aatggcctgc    60

atggcactac attctctggc cctttatcag cactctgaca gctctctcct ttgcttattt   120

tgctcctcat tctagcctct ggatctttgc ccttgctgtt ccttacgctc ttctcccagg   180

gatctgaaag gctcacaccc tcacctcctt cagaggtttg ctaaaatgtc ttctacccag   240

tgaagccttc cccaaccacc acattaaaaa cacacaacca gcacccgttc tctatcttcc   300

ttcactttgc atttgtccat tgtgtaacat cacttacata cctttaattt ttagtttatt   360

aattcatact gcaaaacaac ttagttttta ccatgtgcca ggcattgtcc ctagttgctg   420

acaatacagt tgaaaataaa atagacaaaa atcccatctt ttgaatcttt tgaaccttac   480

attgggagtg acaggcaaaa acgaggtaaa tcagtaaaat acgtgagaca gaacgctaaa   540

agaaaaaaaa gaggaaaggg ctgatttttg tgtcttccct ccaaaatgca agctccttga   600

ggatacagat ttngtgtgtt ttttanttac tgtatctcct gacaatagcg ccccagntcc   660

atagtaaggc attcgatcca attttaaaa atggagatac tagggcagtt tact           714


<210>   168
<211>   792
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(792)
<223>   n is a, g, c or t

<400>   168
ctttcacgag attctgtctc aaaaaaaaaa aaaagccaa agtcctcaaa atggcctgca    60

tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt   120

gctcctcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg   180

atctgaaagg ctcacactct cacctccttc agaggtttgc taaaatgtct tctacccagt   240
```

```
gaagccttcc ccaaccacca cattaaaaac acacaaccag cacccgttct ctatcttcct        300

tcactttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta        360

attcatactg caaaacaact tagtttttac catgtgccag gcattgtccc tagttgctga        420

caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca        480

ttgggagtga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa        540

gaaaaaaaag aggaaagggc tgatttttgt gtcttccctc cagaatgcaa gctccttgag        600

gatacagatt tgtgtgtttt ttactactgt atctcctgac aatagcgccc agtacatagt        660

aggcattcga tccaattttt aaaatgtgat actaggcagt tactcagttt ctgggcacat        720

ttnaactttt agacnataat accgattaaa aaaancggtt ncagctaggc tacgatncaa        780

gananaactg tn                                                           792
```

```
<210>  169
<211>  691
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(691)
<223>  n is a, g, c or t

<400>  169
ctacgaacaa ccatggtgag tagaaccatc tggattttcc atcactttca tttaaaagac         60

tctgttgata ttctaggtac tgattccata tatcagtatc aacaaatttc tcaaccaagg        120

ggataattgg tttatctgtt tgcaattcat tccgtaattt agaaaggaga gaaatagctt        180

tcttttcagc ttccacgcct tcctgcaaaa atacaagaaa aatcaattgt gtgtgtgtct        240

gtgtctgtgt ttgtgtgtgc gtgtctatgc aattcctcta gggtaacata ttttacaga        300

cttaagaaga aaagaaaaat gttcaaacta cattatactt ctttaaacat tacatttaga        360

actcttaaac tgaaaatcaa aaaacacaca cagatctcat atgaacataa tcatgcctta        420

tctatctaag ttctggcctt tctgtgtctt cggtgatcat tactacagag ggaaaggaac        480

ccctgacaga ttttccatgt ctttcatgct tccatacaca ttcttctttc accattgaca        540

ccactagaaa agaaactgtg gcctttctga ggtttctttt ggtagctcaa ttttttttn        600

aacttgtttt ccactgagtt ctagctaggt gagagatgag atatgctgac atacaaggcg        660

ctncaatatt atctnacatg acaggccaat t                                       691
```

```
<210>  170
<211>  699
<212>  DNA
```

```
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(699)

<400>   170
ctcaaaaaaa aaaaaaaagc caaagtcctc aaaacggcct gcatggcact acattctctg      60

gccctttatc agcactctga cagctctctc ctttgcttat tttgctcctc attctagcct     120

ctggatcttt gcccttgctg ttccttacgc tcttctccca gggatctgaa aggctcacac     180

cctcacctcc ttcagaggtt tgctaaaatg tcttctaccc agtgaagcct tccccaacca     240

ccacattaaa aacacacaac cagcacccgt tctctatctt ccttcacttt gcatttgtcc     300

attgtgtaac atcacttaca tacctttaat ttttagttta ttaattcata ctgcaaaaca     360

acttagtttt taccatgtgc caggcattgt ccctagttgc tgacaataca gttgaaaata     420

aaatagacaa aaatcccatc ttttgaatct tttgaacctt acattgggag tgacaggcaa     480

aaacgaggta aatcagtaaa atacgtgaga cagaacgcta aagaaaaaa aagaggaaag     540

ggctgatttt tngtgtcttc cctccagaat gcaagctcct ttgaggatac agatttgngt     600

gtttattact actgaatctc cnggacaaat agcgcccagc acatnagtan gccattcnat     660

ccaatttttn aaaatgagat actagggcag tnactccaa                            699



<210>   171
<211>   767
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(767)
<223>   n is a, g, c or t

<400>   171
catctcacag agttacatct ttcccttcaa gtaatccttt cgctaaggct gttcttgtgg      60

aattggcaaa gcgatatttg gaagcccgta gagggctatg gtgaaaaagg aaatatcttc     120

cgttcaaaac tggaaagaag ctttccgaga aactgctctg tgttctgtga attcctcttt     180

tagaattttc ttcagaactt gtggcacatc attaaacctc cgtcagtgat cacatatctt     240

catcctttgg agtcaattta ttttttggaaa cagtcaaaag tcactcggag tgacttcagt     300

agaatgaagt gtgtgatcaa attggataaa aacttttttt tttaatcaaa aatgagtaac     360

taaaaaaaac agaagactaa attttctttt tgaggcatgt aaactggctc tgaaagaagt     420

tccaaataat tcaaagatgg ttttagcaat ggcagcactg ctgaaatcca tcagtctctc     480
```

```
aaggtgactt aaaaggataa atatcattcg gatgcataga gccaatccgg tccaccacct     540

gttttgtctg actcacatgc taagagtggt ttttatattt ttgaatggct gaaaacaaaa     600

gtgaaagaaa agtagtattt tgtgatacat gaaattcaaa tttcagtgtt cattaaataa     660

agntttcttt agaacacagc catgctcatt cttacatatt atttaaggct gcttttcaca     720

ctacaacgac aggnttcagc agctgcaana aaaaccacat ggcccca                   767
```

<210> 172
<211> 769
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(769)
<223> n is a, g, c or t

<400> 172

```
ctttcacgag attctgtctc aaaaaaaaaa aaaagccaa agtcctcaaa atggcctgca      60

tggcactaca ttctctggcc ctttatcagc actctgacag ctctctcctt tgcttatttt     120

gctcctcatt ctagcctctg gatctttgcc cttgctgttc cttacgctct tctcccaggg     180

atctgaaagg ctcacaccct cacctccttc agaggtttgc taaaatgtct tctacccagt     240

gaagccttcc ccaaccacca cattaaaaac acacaaccag cacccgttct ctatcttcct     300

tcacttttgca tttgtccatt gtgtaacatc acttacatac ctttaatttt tagtttatta     360

attcatactg caaaacaact tagtttttac catgtgccag gcattgtccc tagttgctga     420

caatacagtt gaaaataaaa tagacaaaaa tcccatcttt tgaatctttt gaaccttaca     480

ttgggagtga caggcaaaaa cgaggtaaat cagtaaaata cgtgagacag aacgctaaaa     540

gaaaaaaaag aggaaagggc tgatttttgt gtcttccctc cagaatgcaa gctccttgag     600

gatacagatt tgtgtgtttt ttactactgt atctcctgac aatagcgccc agtacatagt     660

aggcattcga tccnattttt taaatgagat actaggcagt tactcagttt nctgggccca     720

tttcaacttt tagacaataa taccgatnag aaaaacggtt acagctagg                 769
```

<210> 173
<211> 769
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(769)
<223> n is a, g, c or t

<400> 173

```
cagagaacac agnagtcagt ttctcagaaa gcttctttcc agttttgaac ggcaagatat    60

ttcccttttc accatagccc tctatgggct tccaaatatc gctttgccaa ttccacaaga   120

acagccttag cgaaaggctt cttgaaggga aatatgtaac tctgtgagat gaattctacg   180

atacatgtaa cattctacga acaaccatgg tgagtagaac catctggatt ttccatcact   240

ttcatttaaa agactctgtt gatattctag gtactgattc catatatcag tatcaacaaa   300

tttctcaacc aaggggataa ttggtttatc tgtttgcaat tcattccgta atttagaaag   360

gagagaaata gcttcttttt cagcttccac gccttcctgc aaaaatacaa gaaaaatcaa   420

ttgtgtgtgt gtctgtgtct gtgtttgtgt gtgcgtgtct atgcaattcc tctagggtaa   480

catattttta cagacttaag aagaaaagaa aaatgttcaa actacattat acttctttaa   540

acattacatt tagaactctt aaactgaaaa tcaaaaaaca cacacagatc tcatatgaac   600

ataatcatgc cttatctatc taagttctgg cctttctgtg tcttcggtga tcattactac   660

agagggaaag gaacccctga cagattttcc atgtctttca tgcttccata cacattcttt   720

tttcaccatt gacaccactn gaaaagaaac tgtggccttt ctgaggttt                769
```

```
<210>  174
<211>  784
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(784)
<223>  n is a, g, c or t

<400>  174

cttcaaatgt tgaaaaagag ctgaaatgct gcacagctga atgaaggatc ttctcaaggc   120

tctcctggcg cgagccaatc ccagcctcat gaacgagaga gatcctgaca cccacagatg   180

ggcacctcac agccacatgg agacagagac aggctcggtg accagccacc ctcacagcca   240

cacggggaca ggctcggtga ccagccaccc tcacagtcac acggggacag cctcggtgac   300

cagccaccct cacagccaca tgggacaggc tcggtgacca gccaccctca gccacacg    360

gggacaggct cggtgaccag ccaccctcac agccacacgg gacaggctc ggtgaccagc   420

caccctcaca gtcacacggg gacagcctcg gtgaccagcc accctcagag ccacacgggg   480

acaggctcgg tgaccaggca ccctcacagc cacacgggga caggcttggt gaccagccac   540

cctcacagcc acacggggaa cagctctcgg tgaccagcca ccctnagagt aacatgggga   600

caggctcggt tanccagcca cccctcacag ncacacgggg gacnggcctc ggtgaccagc   660

cnacnctnac agncacaccg gggacagggc tnngtttacc agcccacccc tcacagaccn   720
```

cacggggggac agggtttcgt ngaccagccc acccccttaca ntccacacgg nggnacagcc   780

ctcg   784

<210> 175
<211> 733
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(733)
<223> n is a, g, c or t

<400> 175
aatgtgggaa atgcatcatt tgaaacattt taatggagag actagtattt gatatattaa   60

tgttaggttc ctcccagaac ttaattttta aaattttat ccaaacttat tttacttaat   120

tatcaccatt tattgaatac attaattgaa atagctcagc tcttctgacc tgtggagcaa   180

aggnntgacc ctcaggatct cctggaagct gccctcaact aagcagaatt cagaggaaac   240

ttttgactga gaaactgagg tggtcaaatt gtgctaatgt taaaatacat aaaatagaac   300

atttctttca atcagaacta ctgacactat tacatggcac aggttgccag ttactctgat   360

tagaaatact aaacagaaaa aagaaaacac ttggcttgga tccttaaaga ggtatttacg   420

gaaggtgttg ccaacacagc ccatcccaat gtctggtgag atttcctgtc tgggagaggt   480

ctatgggatc tcacccaaac accacagacc ccagtagcat ttcctggact aatgttcttg   540

tcttttcaca gtgctctgct gatttggtct ttagataacn tggtcttcct tcctcttcat   600

aggnatctat accccctgaa gtgtgggtcc ttagactcag ggggcttctt caaaagccct   660

tttggattca gnanaaaaag aancctgggc acttaactgg ggctnaaaga aacacttctn   720

ccgggttccn caa   733

<210> 176
<211> 729
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(729)
<223> n is a, g, c or t

<400> 176
catgtcctttt tcagtaacat ggatgtaatt ggaagccatt attctaagcg acattaatgc   60

aggaaaagaa aatccaatac cacatgttct ctcctgtaaa tcggagctaa acattgggta   120

```
cccagggaca caaagatggg aacaatagac attggggatt ccaaaatatg ggatgtaggg   180

aggagggaaa ggatttataa agtgtctatt gggtactacg tttagtacct gggtgtcgag   240

atcatttgta ccctaaacgt cagcattatg caacatacca atgtaacaaa cctgcacatg   300

tagactctga atctgaaagt tgaaatactt tttaaaagtc tattatatta tcacacaatg   360

accccataaa caacaacaaa aaaaagtgaa agtaaaaaaa cgcaaggtct ttagacgtag   420

gaatcagaat gatataaaga aggaaaagag atttatacta atatagaacc tttttagaca   480

tgaattttaa aaaaatgata cctaggttat caagttactt ttgtgtccac ctaatattta   540

tacactgtat ccctaaccac aattggctgt attttgaaga cagagccctc aaaggaagta   600

attcaggttn tggtgtccct ataaggagga gaacactagn agnatctcag cttctctcca   660

ccccacccccc aaccccaca aaaacatgtt aaagaaagnc tttatnttgn gggacacagt   720

nggagaaaa                                                           729
```

```
<210>    177
<211>    679
<212>    DNA
<213>    Cercopithecus aethiops

<220>
<221>    misc_feature
<222>    (1)..(679)
<223>    n is a, g, c or t

<400>    177
catgcaaggt caggtgcagg catctcttcc aataggggcag tgtctaccag gtagggtctt    60

tctcctctta gaatcattna tggaaatata attcacacaa cataaaattc accctttaaa   120

actatactac acacacacac acacacacac acacacgaat aaaccatatc ccattagcag   180

ttattcaaca cactctgccc ctttgacccc tggaaataat cactaatcta ctggctggta   240

ttatggattt gcttattctg gacaaatcat agaaattgaa tcattaaaca tttggttatt   300

ttgaatctat cttcttttcac ttggcataat gtttgcaagg tttatccatg ttgcagcaag   360

taccaatact cattcctttt tatgcttcca taatattcca tggatatatt ataattttag   420

tcaattttta agtcggtgaa catttacact gtttctcctt tttagctatt atgaataatc   480

ttgctatgaa tattcatgta caagtttttg cataaacacg tttncaattc tctattatgc   540

acctagaagt ggaattggta ggtcatatgg taattctatg ntnaacttt gngaatatat   600

gccaaactat tttccaaagc aactgcaccc atttngtatt accaccatta aggnataaaa   660

ngttcctact ttcttcaca                                                 679
```

```
<210>    178
```

```
<211>  737
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(737)
<223>  n is a, g, c or t

<400>  178
ctttcataat gaaaagaaaa aaatgaattt caactagtat cgatttttcg gtgtgtgggg        60

gcagggcatt taagggtatt atttcctagt aatgatcact tagattctaa gccttaaaca       120

tgattcaaat gcagcagaaa tcaggaaaga agcaacagat acggtggtgc atatcgaatg       180

tctagactac aaggcaaaac ccaaatacca aagaagcatc catgtgtcaa accagcataa       240

tttctaagct atgcctgggg ccacatacaa aaaaaaaaa aaaaaggtta gtttgaaaga       300

aaaatctagg aggggtaacc agaaggtcaa ccccagttca caggaactgg gaagaagcta       360

gccgttaccc tgtgacatct tcctgagcag cttcctccgc agccagctcc ccagcctcct       420

tacaatgttt ccaaaaggcc caactcccta aacatttgct tcttcaaggt catcctaaga       480

taaggcagtg ataaccacc aaacactgag tcacggatac ctttcggcta aaaaagatcc       540

cccttcccaa aatcattaca taaatacttt aaatgccaag agggttttct ccggaactcc       600

accagaaact cccagnactt taatttagat tgggcaacta aatgtgttca antttgcgc       660

cataaaatat taaaggcttt tcaggtctgg caantncagt tcaaaacagg tgctttcagt       720

gtacgctgaa taacagg                                                     737


<210>  179
<211>  759
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(759)
<223>  n is a, g, c or t

<400>  179
cagatttttc tttaagaatt ttgtttattg caataggatt atcaaagtaa aaattaaaaa        60

gtaatgaaaa aattaaaaaa ataattttgt agctaccctt cctataaaac ttatccagat       120

tacttcttga octatacttt gagagcagag gaaatctagc tacattaact cagtagctct       180

gcaacttcta ggtaatttct tacctgaaca gtatatccta agtactgtaa ttcctgcatt       240

gcttgcacat ttgagtttat tattccatcc ctgtattaca ataaatattc tttacataaa       300

ctttcaagag aaaaagcatt caaggtatat gtgtgtgtac acacttatat atatgtgtat       360
```

```
atatactcct gtaaaccata attggagttt aaaaaatata tggtatttgc aattttctct    420

tcttctctc tgtctctctc tctctctctc tctctctctc tctctctttc tttcgatgga    480

gtcttgctct gtcacccagg ttggagtgca gtggtgtgat ttcagcttac tgcaacctcc    540

aactcctggg ttcaagtgat tctcctgcct cagactccca agtagctagg actacaggtg    600

cgtgccacca tgcccggcta attttttgt attttagta gagatggggt ttcaccatgc    660

tgnccagact gntcttgaac tccctgacct tctgatccac ccgcctcgtc ctccnaagtg    720

ctgggataca ggncatgagc caccaccccc gccggtatt                          759
```

```
<210>  180
<211>  770
<212>  DNA
<213>  Cercopithecus aethiops
```

```
<220>
<221>  misc_feature
<222>  (1)..(770)
<223>  n is a, g, c or t
```

```
<400>  180
cagcttttat atatgctgag ttcaagacac ataagtacat atagataant aatgtacact     60

tcttctgtaa gaagacatat aagactgtaa tccatgagag agggaagtct aagatgacat    120

gtttgggaat cctttatatg gacatgatag atgaagccaa agagaacaat gaaatgattc    180

atgttgagtt atttgacatt ttaaaaagta tataagtatt ttaatagtgt gaccatttgt    240

gtctggaaat tttgaaaagc acaaagatct acaatgattt atttatctct atactgatct    300

gtaggaagtt tttggcatgg gaaattgtgc taatgagtat ttggaaacaa gtgtattaag    360

taagggttta caagatcatt agactttcat tttgcagact caatcagatc tgttcactat    420

agtctcctgt tggcataatt ggtttcctga ggacttatta cctgtagatg cacaattttt    480

cattccaaca atgttctgca ttccttttgg actttcctgt cttgaggatc tctttaaaga    540

gctaaaacct caggaacttc ttctacttgt ttctttaaag tcaggatgag agacagaata    600

aggcatccag ccatgatggt ttttccccag gttcttctct catgctaagc cctttatggt    660

acgatgtgcc tctcaaagga gaatgcagat ctaatactat tgcaccactc tgaaagaagt    720

atgaggagaa ggcanaagag ctatgaaaag aaaaacatcc tgatctttt                770
```

```
<210>  181
<211>  706
<212>  DNA
<213>  Cercopithecus aethiops
```

<220>
<221> misc_feature
<222> (1)..(706)
<223> n is a, g, c or t

<400> 181
ctttcatgcc tagtaaagag tggggcttgg cctggagagg gaggcctcat gggccagata   60

agggagatgc tggcccatct gggcacgcat gtgcccgtag gctttccctg tcgagatgat   120

caactggaaa ggcagagaat gcggcctgga ggctcagaaa catccttgaa gccatatccc   180

caggtcctag tcctaactgc cactcttttc ttttttgaa atggggtctt gctatgttgc   240

tcaggctgga ctccaactcc tgggcttaag cgttcctcct gcctcaactg cccaagcagc   300

cacaaaccac acctggcctc ttcctgccac ttctagctta gcaggtggct tcatctgtat   360

acggggatga cgtgactgct tgggggaatg agctgagccc ttggtggaat catggttcat   420

gcaagaggtc tccggcaaaa tgctccaggc ttggagtctg ctgggcgctt ctacccctga   480

caatccgttt acttaccacc accctctgtt cagacaggga agttcttтcc atcaggatta   540

tagcgaggat tggtcttcat ggcacccttg gcatccgagc acgtgttgtt ggagctgttc   600

tacgagccag gacacaccag ggaacggttn cccgcaataa acacccgtct cttcctcgta   660

ctcaagttct tcggggttgc aacattctga gagcttgtcc ttcatt   706

<210> 182
<211> 740
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(740)
<223> n is a, g, c or t

<400> 182
cngngnctcg atcgttcctc ccacctcagc ctcccaaagt gctgtgttac aggtgggagc   60

cactagaccc agctgaatta tggatttta aggctgcttt atgtcaaaca ttgcgggttc   120

tтttaatatt gttttccaga tttaagattt ttttcttta agctttgtat aatttatagt   180

aatttggtaa agtacttttg aaaacaaaaa tgaaaacatt tgcttttctt ctctacctga   240

accctccaga atttagaagc aatttatgat tattcttatt tttacagcaa catggttatt   300

tgcataggtt cagtaagaat ctgttctctg tccaggcaca gtggctcaca cctataatcc   360

cagaactttg ggaggctgag gcaggcagat cacttgagat caggagttca agactagcct   420

ggccaacatg gcgaaaccct gtctctaccg aaaatacaaa aattagcctg gcgtgttggg   480

catgtgcctg gaatcccagc tactagggag gctgagtcag gagaatcact tgaacctgcg   540

```
aggtggaggt tgctgtaagc tgagattgta ccactgcact ccagcctggg tgacagagtg      600

agattttgtc tcaaaaaaaa aaggagggcc aggcatagtg gctcatgcct gtaattccag      660

cactttggga gaccangggg agcgaatcac anggtcagtt cgaggtgact ntaggganaa      720

aattatgttt naatagaaaa                                                 740
```

```
<210>  183
<211>  720
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(720)
<223>  n is a, g, c or t

<400>  183
aaacagtaaa aaataaggaa ttttactttc tctgggcctc ccaggctctc tggttgggtc       60

agggcccaag tggagcaggg aagaaggggc cactctttct gaagtctccc tgcatgaatg      120

aaaataacag ttgagtggca gtcacacact tagaagcaaa tcattctgat tttgccttct      180

agagcagaga tgtctcccct aagatccatt ttaccccagc agaaaaagcc cgggttgtct      240

ggattgtagc aacgctgttt tgacagaaag ccctatgatt tttctcacaa acttccctaa      300

ggatgctatc tttcagctac acatacttag attatttctt ctccctcacc aactcaatct      360

aatgttgcta aggggttcag tactttctct ctgctgctta cctcgtccca accccaagt      420

tctttcccaa attccagcag ctgggaccag tctctgggac agagcagaaa taacatggaa      480

attgggggta gggttaaaca catctatcag tctaggaaca ggtagaaaag caacaccccc      540

gtgactacaa gtttggtagt gggcaacaat tttcttatcc atcatgggtg gtggtgtggg      600

tagtnattga gcataanttt atttgtagag gtgaatttgt ttactgggct ntnaagggtc      660

acatggaggc tgtccaagga aaganattcn ataatnaatg gaaatttatt ataatttaat      720
```

```
<210>  184
<211>  775
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(775)
<223>  n is a, g, c or t

annnnactna nnnnnnnnat tggctnnttn nnttgggggg naanccagta cttcaaaact       60

ttgtattatt taataaatga tactgactag ttggctaaac atttgaacaa aagataaatc      120
```

```
tctaaaccat tctacccacc aaaataaatt ctagaaatga acaaagattt caaagtaaga    180

agtaatccac aaaagtacgg aagaaaacaa tcttaaattg gagaaggact ttctaaacat    240

ggcaccaaag gtagaaacca aaaggaatca cttgcaggtt tcatcacata aagattttaa    300

aatttctata catccaaagc actacaatgt tcagctcaag atggcaggct aggcacattt    360

gcctttcatc tttagagaac catttaaata aaaagacgga ggtacaatga ggaaaaactg    420

taacagggaa gagacgggct ggaacgacag gaagcagatg agccagctgg gagatgaacc    480

agctgaaaga gctgcagtgg agatgaaagc ctgtcctgtg canactgtgg aggaaggagt    540

gaaagacccc acctgtaggt ttggcaagct agctgaggat cgttncncat gattgaacaa    600

natggattgc acnctggttn tccngccnnt tgggtggana ggctnttnnn ntttnantgg    660

nccaacanac antnnnntgt ttnatnccnc cnnntncngn tnnnannnan gggcncccnn    720

tttttnttnn ananccacct nnncnnnncc cnnatnaact nnnnncnang nnnnn         775
```

```
<210> 185
<211> 400
<212> DNA
<213> Cercopithecus aethiops


<220>
<221> misc_feature
<222> (1)..(400)
<223> n is a, g, c or t

<400> 185
tttttcccgg ngggngnnnn nnnnnnnnnn nnnnnnnncc ccccccttn nnnnttgggg      60

ggggggaaan nnccccccc ctttnnnnnn ttttnnnng nnnnngnnac aggttttttg     120

ncgnggggat nntnttancc ccannntttt nnncagnnng gnnnncannc nnnccagcnn    180

ggnngnannn tgctnncctg cncgnnncca gcccgnctct tnncctgnta cagnnnnntc    240

ctnattgnac ctccgnctnt ntatntaaat ggntctctaa agangaaagg caaatntttt    300

tttcctgcca ttttgagcng aacattgnng ngctnnggat gnatagaaat tntaaaanct    360

tnntgtgang aaaccngcaa gtgntttttt tnnggnncct                         400
```

```
<210> 186
<211> 951
<212> DNA
<213> Cercopithecus aethiops


<220>
<221> misc_feature
<222> (1)..(951)
<223> n is a, g, c or t
```

<400> 186

```
ccgccnggtg ntgggaaaga cnnnggacgc ttcagaccac aggnaggtac catcctggaa      60

cctggaatct ggaacctcag gggctgacct ggcactgggt gggcctggaa cctgtatctg     120

cagcccagaa gcagggtctg caggtgcaag cctgatgcca ggctgcaggg gacagccgng     180

agcnggtttt tnttgaggca ggggntgata angccagcag gcccaaagca aagnctaggg     240

cnnatntntg tctcctaccc ccatgcngag gatacctnnn ttnaagctgc ggagccngag     300

gaagggaggg ggcgcangca agagaatgtc anaactancc ttncnnacct nctncagngc     360

nacctccagg ngctgtaanc actcactagg anacccttaa ggncnnactg aaaggagcnt     420

ccctangagn gatggnagca aaaaananga nacgacactn cgactgcnng gngacgtgca     480

acntggaaag actctgnncc ctncancacc tcgggnanac tatnacaaag angncccca     540

ncacctncan aatgaaagna aangtgancg ngcnanacca acnncgacnn ccctnggcca     600

agagaacacc aataacnaga ntagganatc caaaagcggn aaanacnaca gngctatnng     660

gaatgcncaa gccaccatnn cttgcantgg nncaacagnt gnaatcnaaa nctacnnccn     720

cnatacactg gagagacaan naccnagcnc cantaaagcg nnaaaaanga gaaaacgnaa     780

aaaancgcgc anngnngcng ncnaatngcc cnnaccntaa ccctccnnan aaaaannaat     840

cnngaacctg gnnacgacnn ncnaagnggc ncaanccncc cncaggcgnc tcnnccncct     900

gccacnanca ccccngagcc ncnncagagn caccngcctn acncacccan c              951
```

<211> 450
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(450)
<223> n is a, g, c or t

<400> 187

```
tnctnntttn ggggtnnnan nnnnnnnnnn anntccncca atnnnnntgg gggggaannc      60

ctggtttcct gcactctccc tcttttccac tcatgtcgcc aggcttccca aatgttccct     120

gactattctt tccctttttt gtgcccacct gtgccccagg cacagcatgt gacctagtcc     180

tgggagtccg cggtggcaga actgcaggcc gttggggcct ccaagtagac catgcaagtt     240

tcacagccat attnctctga tatcagaagc taaggagtcg tgcctggcca gtactaggat     300

 gggggtccgn ctgggaacac tgggtgatgt aggctttttg cttacagnnc cctccctctn     360

tccccctnca gnngnctnga tncacaacca tnccctgact ntnntntncn ntnnnnncac     420

gcaactgcat ncnanacaca nncngngact                                      450
```

<210> 188
<211> 338
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(338)
<223> n is a, g, c or t

<400> 188

```
tncnncttnt ggnggannna nncnnnnnnn nnnntcccnc ctnnnntggg gggggaannc          60

gnncacntnc nntttangaa agagacgacg cttncgagga agaaggtttn tgggacgcgg         120

gactgggnag agctccagag ccccagcagc ccggctcaag gncccctgcg cataggcgcc         180

ccaccgngac gncagggacg cgactnccgn gangccccgc gcgccgnnng ancccaggcg         240

cgggcnnaga ctgngatcnn ggagnngccc ngngccnnnc ngacggngcg nnnnggnggn         300

cnngggcgcg ggcnnngnga nnggacagnc nggagcnt                                 338
```


<210> 189
<211> 936
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(936)
<223> n is a, g, c or t

<400> 189

```
ttttnngggg gaannnnnnn nggngtangn nnnnnnnccn ccgcggttnn nccttggggg          60

gggaannncc nnnccangtn ncttttttcat gnaaagngna cgacgntctc cgaggaagaa        120

ggctccggga cgcgggactg ggtagagctc cagagcccca gcagcccggc tcaaggtccc        180

ctgcgcatag gcgccccacc gtgacgtcag ggacgcgact cccgcgatgc cccgcgcgcc        240

gtctgatccc aggcgcgggc tcannntttt atctcggagt tcccctgcgc cttcctgacg        300

gtgcgttctg gcggcctcgg gcgcgggctc tgcgatcgga cagcctggag cctttggcct        360

cgatttacat gggaggcccc tcgaaacagg gcacgtcact tgcccccggt cacctgcgga        420

cggggagact ctcgggttga ctccaaggcc tgacattccc ctccggtttt caccgaggag        480

gatgaggatg ttgtcaggag ctgcggcaag gctggaggag cttgcgttgn gtccacccnc        540

ctctgnacag gccttagcat ncacccncag tttctccctt gacttntgaa cccnaactcc        600

ttaccccgc aagtnncnnc cctgtttnga ttgctgaaac tgcaagtgac ggaagantaa        660

aatgtttgcc naagcntnat gcttnanggn ggntgccngg gtataaggtc angggttggg        720
```

124

```
ggcccttnnc cctgnngggt nggcnttaag ntaacccagg gnncntggca nttnantnnt      780

attcaanana tgccanggnn ntcggnntnn aanggntntt tnnanaaaat nnttnccctt      840

nttannctnt annccnnagg gaaanccntn gggtcttgtt tngccctgna aanacnatna      900

aaggggtaat nncccncnct tnaatntnnn gncncc                               936
```

```
<210>    190
<211>    936
<212>    DNA
<213>    Cercopithecus aethiops


<220>
<221>    misc_feature
<222>    (1)..(936)
<223>    n is a, g, c or t

<400>    190
tttttnngng gannncnnnn gtttntngnn nncccccccc ccatnnnttt nggggggggaa      60

nncccnnnca cgtcctcntn atgaaagaga cgacgcctcc gagaagaagg ctctgggtac     120

gcgggactgg gtagagctcc agagccccag cagcccggct caaggtcccc tgcgcatagg     180

cgccccaccg tgacgtcagg gacgcgactc ccgcgatgcc ccgcgcgccg tctgatccca     240

ggcgcgggct cagantnnna tctcggagtt cccctgcgcc ttcctgacgg tgcgttctgg     300

cggcctcggg cgcgggctct gcgatcggac agcctggagc ctttggcctc gatttacatg     360

ggaggcccct cgaaacaggg cacgtcactt gccccggtc acctgcggac ggggagactc      420

tcgggttgac tccaaggcct gacattcccc tccggttttc accgaggagg atgaggatgt     480

tgtcaggagc tgcggcaagg ctggaggagc ttgcgttggg tccacccgcc tctggacagg     540

ccttagcatt cacccgcagt ttctccctga ctttgaaccc aaactcccta cccccgcaag     600

tccttccctg ttttgattgc tgaactgcaa gtgacggaag aattaagtgt tggccgaaag     660

ctgatgcttc aggggggtgca ggntagaggt caggggtggg ggcctngcct tgnggngngc     720

atantgtanc ccanggtccn gcactgantn ttnnaggaat gcanggaatn gnatannang     780

gtnctaanaa antntccccc tannaactga taccnnagna accntngggc tgnntgancn     840

tgaaaaaccc annagggtaa ngcctnnctt atnngggccc cnntntcnag annaaangcc     900

ctggggtttc anngaaaacc cnnnnanaaa ntntgg                              936
```

```
<210>    191
<211>    951
<212>    DNA
<213>    Cercopithecus aethiops
```

125

```
<220>
<221> misc_feature
<222> (1)..(951)
<223> n is a, g, c or t

<400> 191
ttttttnngng gancnnncng gttgttgnnc cntcccgcgc attcccttgg gggggnaacc      60

cccnnncang tncctnttna tgaaagagac gacgcntccg agaagaaggc tctgggacgc     120

gggactgggt agagctccag agccccagca gcccggctca aggtcccctg cgcataggcg     180

ccccaccgtg acgtcaggga cgcgactccc gngatgcccc gcgcgccgtc tgatcccagg     240

cgcgggctca nanttnnatc tcggagttcc cctgcgcctt cctgacggtg cgttctggcg     300

gcctcgggcg cgggctctgc gatcggacag cctggagcct ttggcctcga tttacatggg     360

aggcccctcg aaacagggca cgtcacttgc ccccggtcac ctgcggacgg ggagactctc     420

gggttgactc caaggcctga cattcccctc cggttttcac cgaggaggat gaggatgttg     480

tcaggagctg cggcaaggct ggaggagctt gcgttgggtc cacccgcctc tggacaggcc     540

ttagcattca cccgcagttt ctccctgact ttgaacccaa actccctacc cccgcaagtc     600

cttccctgtt tgattgctga actgcaagtg acggaagaat taagtgttgg cgaaagctga     660

tgcttcaggg ggntgcaggg tagaggtcag gggtgggggc ctcgccttgt ggngtgcata     720

tgtagcccag ggtcntggca ctgattntta ttaggaatgc aggganttng attagatggt     780

ttcttagaaa atatcccctn tgnanctgnt acctgagnaa ccgctgggct ggcatnacct     840

tgnaaaaccc agaanggtta nngcccttc ttantngtgg cccnatttttt tcaggacnaa     900

angggccntg gntttncaat gnaatcncnt ttgcncaaan nnctggtttc t              951


<210>   192
<211>   938
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221> misc_feature
<222> (1)..(938)
<223> n is a, g, c or t

<400> 192
ttcnnggntc ttnntgntan attttcccc ccattttttg ggggggaanc cnacncanca       60

aaaggtagaa attattgata aantntaaat gttacaaact gcngctaaaa gaagcaaaag     120

agaacatgct gtatgatcct ttttttttt tttttttttt ttttttgag gcggagtttc     180

actcttgttg cccaggctgg agtacaatgg cacaatctcg gctcaccaca acctctgcct     240

cnnnttttca agcaattttt ntnncttann ctccctagta gctgggatta taggcatgtg     300
```

126

ccaccaggcc cagctaattt tgtattttta gtagagacgg ggtttctcca tgttggtcag   360

gctggtcttg aactcccgac ctcaggtgat ccaaccgcct cggcctccca aagtgctggg   420

attacagacg tgagccactg tgcccggcaa tctttttttct taattttaaa ttttttagag   480

acaaagtctg gcttttctag tnccaggctg gagggcagtg gagccatcct ggctcactgc   540

anccttnnc tcccaggctc aagccatcct nctaccttaa ncttcctgag tngctggnaa   600

ctacaggtac acaccaccat gtcagnctaa tttttttttt tttttttttt ttgaaaccna   660

atttttttcnt tgttcacccc tnntgganan ncaggnngna nnanctctnn ccncntcnac   720

cccttacnnc naagnncaat atnaantatc nncctacnnn ccnagntct tnnnntttta   780

annnannttn tatttttntt nnttatantt tacctnnntn tttcntnntn ctnanccctn   840

ntncactnnt nnactantct ttttccacnt attcttctct ncnnctntnc tnatatcncn   900

nnccnnnctc tctcttntnc ttctttnttt ctnnnatn   938

<210>   193
<211>   804
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(804)
<223>   n is a, g, c or t

<400>   193
tntnggggt nnnaaaacnt tncnnacata atcgccncaa tacaanttgg gnggggaaaa   60

annctgnntc attcctccnt gnacccatct ccatgccgtg naagcatctc ctncttggac   120

ttgcactatc tggtcccata gcccttgctt attcttaaat gggagtcact ctgacttgca   180

ttgtggggaa gggtatacct ggggcacagt cctctgggat ggacacttcc ataggaaggg   240

gcagttatac gtggacttat gtcctcctac actctcatcc agaaccatcc acccagaagc   300

aggagttgtt tcttttagaa accagccggc ccaatcagcc cattttatag gtgaaggcag   360

tgaagcccag agagataaag catcttgtcc aaggtcacag agccagacct agactaggct   420

gcctggctcc tagttcaggg ctcatcccac cctagccggc ttctggctag acagaatcta   480

cccatcctgg cccagactct ctggtgggaa gtcagggatg cagnggtcag gatgggcatc   540

agagccagca ggccctgagc acggntcacc caagtggaac atgaacttcc taaactccag   600

nggaagttag aaatggcana ttgatcagng ctaatgagct taaaacaccc agggattaaa   660

aaaaaaaaca tgaanaagct ntacttnaag cataaatntg ntnaacanaa agganaccng   720

gctncncnnt ntntnanann nacnnnntgg aggctnaggg ggnnngnnca tnngggngngn   780

ganattngnn ttngnaaggg gnnt   804

<210>   194
<211>   560
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(560)
<223>   n is a, g, c or t

<400>   194
ttctanttnn nnnggtnnna ancannnnnn ncatnntcgn cncatnnnnn ttgggaggga   60

aannnaatna ataatcaaan ttagnaattg aatttagaat ttcatttatg aataaaaagg   120

ctgggaggaa acacacccca accgacacag tggatgcgat aggataagac tatgagcaga   180

ttttgttctt ccttttcacc gtctgtattt tccatcaatt atttgtatga ttaaaatcaa   240

tcatttcaga caagagggac attgtgagct atctgtgaga aatgtcttct atctgtttcc   300

agatagaagg ggctccagct cggtttgggg aaagtcccaa tgccattctc ttaaccaaga   360

ggtttcctac ctcatctaat gtggagattc tacttacccg ggaagactcc cctcctgtta   420

cctcaagtct gcagccggcc tcccagactt ctgcctnctn ctaaccacag cctgcctggn   480

tgcaggncgg ngggaaagga gggcatangg ggctgnatnc cgnanaggcc ctnncactcc   540

tngactnang cagggnnctg   560

<210>   195
<211>   977
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(977)
<223>   n is a, g, c or t

<400>   195
cnnccccccng gntnccccncg ggnnnnnnnn nnnnccccccc ccnannncttt gggggggaan   60

nncnnnccttt tnggngnatt gnngggnana anncngtnct tccnnaatag natgnggcng   120

canttcaact ncgctaatta acggaacagc aggctngnaa ttctgacaac agcaggacac   180

aaanggggcn gggatcagca ctgaatgccg gcgaagcatg ccnccccccc ttaagaagaa   240

gcacaacacc cacgacccac attnnntntn gggncaggtc catgaaggng cnaccctnga   300

tttagttana ngcnctnccc tgcagcaact ccaagggcnc agggtttttta aaatgncncc   360

tcaggccttc ttnagaggna gcaagccngc cccaactggc cttttttcnna aaaagangg   420

128

```
aaacaggnct gngattggtc nagagcagga nncgcccagc ccnttnggct cccgngggcc      480

acacngnaag aaaaagaatn gnnttggacc acacagaaaa cacaccaana ctaangacag      540

ctgaaaagct caaaaaaaaa atcgcnaaaa aatccctcaa tgctcnaaga agtccncaaa      600

nncgccgngn gacngnnaca cagctnccng gccngcanga cnncnggggn ncacaggnng      660

cnacacccag gaccagnagn taatatcnna aaagggtaac aanaaaancc ctaataccaa      720

aaangcnatg anaatggaag cnnnacntcc tncaaaagac aagccctang gaaancntcn      780

cncnacccnn ncccaaccn ggcanncggg cccccaccca aagggggggn nccgccccgg       840

aannnaaaan ccnacnnngg ggaaaaanng accnnaancc ngaaanngtc tatanccca       900

cngnccnaaa acctcccang ncaatnaccc cncccctccta aaaggntagg annaanacnc     960

nggngcaaag ncnnncca                                                    977
```

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<210>  196
<211>  868
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(868)
<223>  n is a, g, c or t

<400>  196
gaanncnnc nnaaaaaacn nnnnncccc nccccatann ncttgggggg gaaannnccc       60

ccccacaagn natantnagn aggnaggaaa acacanttaa tatatctcac tagcnctcat     120

ttccctcccc caccctcatc ccactccact gctaagagag agaaatnnca gcactgctat     180

cctgttntat tatacattnt cccttnngag tnaaggattn naagattnng aaagtaacag     240

aatagaaacc aaaagtnnta ctcaactncc aatttggctt aaaaagagag aaataatnat     300

tattncctat gnnacccaaa actnattctg nnaataacag ntataattat atattcaaan    360

naataaatga agatcgccaa aatcacctna atataatngn nagcagctaa agaacaaaaa    420

tnnnnnncat nngctnctat aagnagacat cacatganna ctnctatnga ccagnaagaa    480

actagnaaaa ncaggcagnc acccaccatn cnnnnctaac annennnnnc nnannctatn    540

caaccnnnnc ggnatanncn naagaagcca aatcaagaaa nnagaccnnc atgcctaaaa    600

aaaaanngng nnatcnnaan acatcangaa caggaaccng nngnanataa cacaggnann    660

caaagcnnna ncgncaannn cnagaacccn naaacanaaa ggcagcnnan anncaagann    720

agaaacngaa nncacanaac acanagcann nncncanaaa gcnnnnnnca nnnnngaacg    780

aagaaannnc nnnnnaccaa aggccncaag ggcnnncaaa nnccnnngcc aannnaaaaa    840
```

aaaccnanca aaggcncnng anggaaaa   868

<210> 197
<211> 260
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(260)
<223> n is a, g, c or t

<400> 197
ttttcnggng gannnnnnnn nnnnnnnnnn nccncnccgn tnnnnttggg ggggaaannc   60

nnnncacang nnatnttngn ggaggaaaac acatttaata nanctcatta gccctcattt   120

ccctcccccca ccctcatccc actccacngn taagagagag aaatnncagc actgntatcc   180

tgnnnnatna tacatttncc ctnnngagtn aaggatnnna agatnnngaa agnaacagaa   240

nagaaaccaa atnttttttt   260

<210> 198
<211> 901
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(901)
<223> n is a, g, c or t

<400> 198
gggnancnnn agnngnaana nnccaacccc gccaanatnt anggggggan actntcacaa   60

gtatacaaga ggaggaaaac acaattaata tatctcacta gcattcattt ccctccccca   120

ccctcatccc actccactgc taagagagag aaatttnggc actgctatcc tgttntatna   180

tacatnttcc cttttgagtn aaggattnna agattntgaa agtaacagaa tagaaaccaa   240

aagtttnctc aactnccaan nnggctaaaa agagagaaat aatnattatt tcctatgnna   300

cccaaaactn anncngnnaa taacagntat aattatatat ncaaatcaat aaatgaagan   360

cgccaaaatc accttaatat aattgncagc agctaaagaa caaaaanncn ncncannngc   420

nncnataagn anacatcaca tgatnactnc tatngaccag naagaaacta gnaaaancag   480

gcagncaccc acccacncnn nnctaacatt cnnnnncnna nncnanccaa cctnnnncgg   540

natatncnna agaagccaaa ncaagaaaan nagaccnnca ngccnaaaaa aaaacngngn   600

nancnnaaac atcangaaca ggaaaccagn ngnaaaataa cacagggnat ncaaaagcnn   660

```
tanccggcan nnnnccaaaa acccctaaac anaaaaggcn gncccagaac ccangaaana    720

gaaaaccnga aanncccngg nnaancccgg cancnncccc caatccacaa cccccgnna    780

naancnccn aaacccancc aaaacanaaa acccngnggc naaaaaggcn ccccnaaaaa    840

aanggnnccc cggnccggcg gncgaacncc cnagggncaa nannggggng nagncaaaaa    900

a                                                                  901
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<210> 199
<211> 885
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(885)
<223> n is a, g, c or t

<400> 199
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ttttttnggn ggntttnnnc nnttttnntc nnnnnncccc cccgattnnn nttnggggggg    60

aaannnccnn nccanaagnn atnttagnag gaggaaaaca canttaatat atctcactag    120

cattcatttc cctcccccac cctcatccca ctccactgct aagagagaga aatttcagca    180

ctgctatcct gttttattat acattttccc ttttgagtta aggattttaa gattttgaaa    240

gtaacagaat agaaaccaaa attttnntca acttccaatt tggctnaaaa agagagaaat    300

aattattatt tcctatgtta cccaaaactt attctgttaa taacagttat nattatatat    360

tcaaattaat aaatgaagat cgccaaaatc accttaatat aattgttagc agctaaagaa    420

caaaaatttt tttcatttgc ttctataagt agacatcaca tgattacttc tattgaccag    480

taagaaacta gtaaatcag gcagtcaccc accattcttt tctaacattc ttttncttat    540

tctatncaac ctttncngta tattcttaan aagccaaatc aanaaatnan accttcatgc    600

ctaaaataaa attgtgntat cttatacatn atgaacagga acctgtngta tataacacaa    660

nntatnncaa agctttatcn cantttctan aacccttaaa caaaaangca nnctcanatt    720

nnaanattan aaaactnaat tctggaccca antgtanatt aactctnnan acatttttnn    780

gtgnattaan naaaaactgg nnncctatcc ttaactttaa naggtcancc caaanttntn    840

nnanaacaan ncctnnnnan aancaantta tatnaaacca nctan                  885
```

<210> 200
<211> 941
<212> DNA
<213> Cercopithecus aethiops

<220>

<221> misc_feature
<222> (1)..(941)
<223> n is a, g, c or t

<400> 200
ttttnggggg anntananng nnnnnnnnnn nnccnngnnn nnattggggg gaaannnccn   60
nncttngnat ttagaggagg aaaacacntt taatggatct tattagcttc atttccctcc   120
cccaccctca tcccactcca cngntaagag agagaaattt cagcactgct atcctgtttt   180
atnatacatt ttccpttttg agtnaaggat nntaagattn ngaaagtaac agaanagaaa   240
ccaanntttt ttttcaactg gnaattnggc tcaaaaagag agaaataatt atnatntcct   300
atgttaccca aaactnatcc tgnnaataac agttatnttt atatattcaa attaataaat   360
gaagatcgcc aaaatcacct taatataatn gncagcanan aaagaacaaa aatnctttca   420
nncngcttna ataangnnga catcnccatg atcacctnct attgaccagn aagnaaacta   480
gnnnnaatna ggcnanncac ncacnanann nanncnaanc accannnnna cnaannncna   540
ttcaacannt nannggnana ntnncnnaat aagccnaaat aanananann gccccnanan   600
gcctaannan nancgaggna atgcnnnncc caannttnaa caggnatncc nggcagngnt   660
tntaacanng annatttcan angnnnnanc cggnaatact nnnanaannc cnannaaann   720
naaaggnnan tcnnaatnca angttnaana aaangnaatn cncccnnnnn antantaaat   780
aangncnnna ntannannnn nctancatcn cncncnatgc acnnnnnaaa ntnnnnnntn   840
acnnncnnnc nnngnnaaan nttnaangga nnncnnnntn ancacannnn cncannaang   900
nnnnnnaana nccacaannc aacacatnan caancacnaa t   941

<210> 201
<211> 886
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(886)
<223> n is a, g, c or t

<400> 201
ttttcccnng gntnnnnnnt nnnnannnnn nntccccccc catnnnnttt gggggggaaa   60
ancacagnaa cacagngttt nngnnctcag naaagctttt ttccagtttt gaacgtaaga   120
tattcccttt ttcaccatat ccctctatgg gcttccaaat atccctttgc caattccaca   180
agaacagcct tagcgaaagg cttcttgaag ggaaagatgt aactctgtga gatgaattca   240
cagaacacaa agcagttttt ttagaaagct tctttctagt tttgatctga gaatatttcc   300
cttttcacca tagacctcta tgggcttcca aatatcacgt tggaaatttc acaagaacag   360

```
tgttagcgaa aagcttcttg agggaaaagc tataactctg tgagatgaat tctacgatac      420

atgtaacatt ctacgaacaa ccatggtgag tagaaccatc tggattttcc atcactttca      480

tttaaaagac tctgttgata ttctaggtac tgattccata tatcantatc aacaaatttc      540

tcaaccaagg ggataattgg ttnatctgnt tgcaaantca ttccgtnatt tnanaaaagg      600

agagaaaata gctttctntt cancttncca cgccttncct gccaaaaatn ccaanaaaaa      660

ancaatngng nngnggngcc ncgnntnntg nngnttngng tgtnccntgn nctntccnan      720

tcccnntnag ggnnaacnaa tttttncnga ctttaanaaa naaaanaaaa aanngnncaa      780

accacnttnn aaactnnttt aaanntncca tnnnaaacct taaancnnaa aaccaaaaaa      840

anccccacn ancnnnnnnn nanananann nnncccntan ttnttt                      886
```

<210>   202
<211>   925
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(925)
<223>   n is a, g, c or t

<400>   202

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tttntggng gannnctnnt nnnnnnnttn nnccccncct annncttngg ggggaannnn       60

cnnccocactt agnatttttt ncncaaaaaa aaaaaaatag ccaaagtcct caaaacggcc    120

tgcatggcac tacattctct ggccctttat cagcactctg acagctctct cctttgctta    180

ttttgctcct cattctagcc tctggatctt tgcccttgct gttccttacg ctcttctccc    240

agggatctga aanntttttt tccctcacct ccttcagagg tttgctaaaa tgtcttctac    300

ccagngaagc cttccccaac caccacatta aaaacacaca accntttccc gttctctatc    360

ttccttcact tngcatatgt ccattgngta acatcactta cataccttna attntnagct    420

natnaatnca tactncaaaa caccttatnt nttaccatgt nccaagcatt gnccocntant   480

tgcttnacan tacancncna anatnaaatt cnacanaaaa tcccatnctt tttgaatntt    540

tttgaacctt acattngnaa gtnncannca aaatccnang ttaaancata aaaatncccn    600

tgnanacnna acccctnaaa naaanaaaat angaaganag gggcctgaat tnnngngcnc    660

tttcccctcc caaantncan acntcctngn angnaaccnn atctnnnnng nnntnnnntc    720

actnccgtnt nttcccgaca anaancnccc cnnnnccctn ntnngccctt ccatnccnat    780

tnttnaaana ttaaaanccc cccncnctcn ctaanttnct ngggnccnat ttcaaacttt    840

tnaacnaann annccnncc nnnaaaaacn ncnnccnccc tnngnnnccc anncnaaatc     900
```

atccnncntc nnctcctcnt ctccn   925

<210> 203
<211> 895
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(895)
<223> n is a, g, c or t

<400> 203
tttttttcgng gattnctnnt ntnnnnntnn ntcccccat tnnncttggg gggnaannnc   60

nacgattcan gtnttatnnc tacgaacaac cattgtgagt agaaccatct ggattttnca   120

tcactttcat ttaaaagact ctgttgatat tctaggtact gattccatat atcagtatca   180

acaaatttct caaccaaggg gataattggt ttatctgttt gcaattcatt ccgtaattta   240

gaaaggagan anntttcttt cttttcagct tccacgcctt cctgcaaaaa tacaagaaaa   300

atcaattgtg tgtgtgtctg tgtctgtgtt tgtgtgtgcn tgtctatgca attcctctag   360

ggtaacatat ttttacagac ttaagaagaa aagaaaaatg ttcaaactac attatacttc   420

tttaaacatt acatttagaa ctcttaaact gaaaatcaaa aaacacacac agatctcata   480

tgaacataat catgccttat ctatctaagt tctggccttt ctgtgtcttc ggtgatcatt   540

actacagagg gaaaggaacc cctgacagat tttccatgtn ttttcatgct tccatacaca   600

ttnttctttc accattgaca ccnactanaa aaagadaccn gtggnccttt ctgaggtttt   660

ttttttngnn anntnaattn ntttttttta aacttggntt ttccncctna attnttancn   720

taggntnana aaangaaana ntgcctnnna tnaaaanggn ncctncaatn ntatnttacn   780

cnnanaagnc cnattggnna gggngcanaa antntnanng ggnnacnaaa ataaaannaa   840

aaataactct nnnancctttt ggttttacat taacnaaana nntctncccc caana   895

<210> 204
<211> 887
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(887)
<223> n is a, g, c or t

<400> 204
ttttcnngng gntnnnnnnn nnnnnnnnnn nnaccccncg tnnnnntngg ggggaannnc   60

cnncccacga gnatttttnn ctcaaaaaaa aaaaaaaagc caaagtcctc aaaatggcct   120

                               134

```
gcatggcact acattctctg gcccttatc agcactctga cagctctctc ctttgcttat      180

tttgctcctc attctagcct ctggatcttt gcccttgctg ttccttacgc tcttctccca      240

gggatctgaa aggnttacac cctcacctcc ttcagaggtt tgctaaaatg tcttctaccc      300

agngaagcct tccccaacca ccacattaaa aacacacaac cagcacccgt tctctatctt      360

ccttcacttt gcattngncc attgngtaac atcacttaca taccttnaat tnttagttna      420

ttaattcata ctgcaaaaca acttantttt taccatgtgc caggcattgn ccctagttgc      480

tgacaataca gnngaaaata aaatagacaa aaatcccatc tttngaatct ttngaacctt      540

acattgggag tgacaggcaa aaacgaggna aatcagnaaa atacgtgaga cagaacgcta      600

aaagaaaaaa aagaggaaag ggctganntt ngngncttcc ctccanaatg caagctcctn      660

gagaatacag annngngngn nnnnnacnac ngnatctccn gacaatagcn cccannacan      720

annangcatt ncacccaan tnnaaaaang annaacnang gcannnnccn aannncnggc      780
cacatnncaa ccntaaaaca anaanaccca anaaaaaaac ngnnncagcn aggncacnaa      840

nnaagaaana nccgnncnna attnnnggng caggccntna aanncca                   887
```

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<210>  205
<211>  843
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(843)
<223>  n is a, g, c or t

<400>  205
acccccccca tnnnnttggg ggggaaaaac canccagtaa nagttttgnn gcaaggnngg      60

tggctcttaa tcatcagggg caaggtagat ttaattctcc attatccatt aattatttaa      120

tgaacaccaa cagtgggatt gcaagtggga ggtttagaac aacagggctc tgtggcaaag      180

actactagac catggtatca ctagggacag ctagttgggg aggcnttnng ggtattactt      240

ggcttataaa accaaaatag accaacagca gattattaaa atgctggtgt tggctgccaa      300

gtggaacgta ataatcacac atctggtttt ccaaattgaa cagttcttag atccagaatc      360

ctgtgattga tagagatgct agatcctttt gcagaaaatc ttataatgcc ccaatgaatt      420

tatagtagta atttccccaa tccttctcca aaagaatcta tgctgcagaa aataaaatac      480

ctgnacagng ngcattacat tgngcactac agagatgaaa gtagccaaat atttcaagtg      540

ctgnngaatc canagttnga gatgacacca ataccagaga aaacaaaaac catcatgatg      600

ccctggntag ggngggtgtg ngaaanccan gnggaaaaan aaagncttgg gcccnacant      660
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ncanatataa atgnncaaag agncnggcna cccnccccgn naanaaggnn agggncnctg   720

nnggccnaaa nnaggnnngg aagcaccnaa anaannngaa anaaccccc accaaaaccc   780

ccgngcnccn gaccnggana ggggggnncc cntncncann ccaaaanggc ccannggnnn   840

ncc   843

<210> 206
<211> 927
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(927)
<223> n is a, g, c or t

<400> 206
ncnccccng gnaanccccn ggngtaannn nnnncccccc ccaatanntt tggggggggna   60

annncccnnn canagtgnaa tantaagnaa ncaaaggcag cngagtcagn accaaaacta   120

acagnanaat aacagnaaaa nnnccaccac catatgaaag caggggaaaa atatatggaa   180

acagatatgg ccaaaaaaaa ggatgcagac aacgaagnaa gcggacagaa gcccgagaag   240

aaaaacgggg ncgggggaga aaggagacta tnaataggaa aaangaaaaa gcanacacag   300

ggcgactgag caatacagaa agcaaagang cnggataaaa agcagggccc tagagtggga   360

gtggcncaac acgaagaggg gcatccagag ggggaataca gcgcngggng acaggagggg   420

gnccaaaang gaggaaaagc gcccnncnca gagaaccanc aggcgcggcc caccccggggg   480

cggcagccgg ggaggggggcc cacagangng ggngagaagc caagaaacnc agcgganggn   540

agggaancac nggcccangc gcaggggaca cccccccagaa gccnaggaca gagggagggg   600

caaggngcac actaagganc cnnnaangaa cggccagagg ngcaggancc cacannagaa   660

gnacccngaa ggggcaggng caggcaagnc cccgcngcan gaggacaaaa cnggccngcn   720

gaaaanggnc gccccnncac cccnccngnc cnnaacccac ngcaaccacc agncnnnnac   780

annaanccccn aaaacacaaa ngnccccacn nnanccancc cganaaaagg cnaanaacca   840

gggngnaancc nacccaccng gnccgnanga cccnggaaac cnnnanncca nncnnaannn   900

nnacccnaaa ccaaaagnnc gannacc   927

<210> 207
<211> 940
<212> DNA
<213> Cercopithecus aethiops

<220>

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<221> misc_feature
<222> (1)..(940)
<223> n is a, g, c or t

<400> 207
ccccggnatc ntttctgtnt nntnctnnnc ccccccctta ttttggggggg ggaannnccn      60

nnncntnnnn nnntttncca ccnaaaacta tttnttntnc tnncccgcct atcctccaaa     120

ctagcaatan ttcggttctt ccctcttgct ctcgggcgga ttcctgaaag tcgtttattc     180

tcttaattaa tacgccgctc cagccccgcc cgttcagctc attctcttaa tcgcattacc     240

ctggctgcng nnnctttttt ttttttccac ctgctgccac ccacccagac accgcctncg     300

gctctttccg gaccatctca gtttctcctc cttccccngn cccaattttc tttaggctat     360

ttctggctcc cgtaggtttn tcatgctctc gttagcccca ccccatcacc accancggct     420

ctttttcggc tctctcccgn cncctcctgt ctcctgctca ggctcttttc cagctattnn     480

cgactcccct cntactcacc ctttgccttc ngaaactntc ccaccngccc ttcaggcaaa     540

tcngtctcna ccccctantc ccgcacgtga acacagncct nccccctccg ccttcttaga     600

naccccctct caccnnnncc ctttccnncc catcctcaaa actananggn tgggtacngg     660

ccnanccncc cnttttggtg nnnaannccn gaatcgccgn caaggncccg gtncntnccc     720

ngaaaancct atngncnggn cacaaacang ggaaacannn ttcncacccn ttntccactg     780

anccncttcc cccntcaccc ttnaaanaca ttntttnnnt ttatctaaaa ccnttcancc     840

cccncctcct tcggncacct cnttnctant ncccatatan ccccntagnt natncntnca     900

atnccngcac cnnntntnta tctaatnaaa ccccaacccc                           940


<210>  208
<211>  881
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(881)
<223>  n is a, g, c or t

<400>  208
tttttccnng gnnattcnnt gtnnaatntn ntntcccccc cattntttgg gggggaanac      60

ccgnanttga aatttnggga caaacaaaca tanctctttc tctttccttg aagggttaat     120

gctccaacca gcctcagatt ggttcgcttg aatcttaaaa ttactttttct ggtcacgcgc     180

gccgaaggtc taagcatttg tgaaatgtct tttttccccc ccccacccc ttgatgctgt     240

tctctttggn nttttttaat tacacagggg ttgagaaacc aaattaaaat taggcgtgtc     300

tggtcaacag tgatcacgtt gcatgctttt agctttgntt gttgaagttg cttctcctcc     360
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137

ctgagtggct ttcctccttt tttttttttt tttttattt taaaaaggaa atatcataag   420

ctctttcaga aatactcaca ggaagtgagt gtccgtatgc tggttactca ccancaactg   480

agtgttggca ggtggagaat gctaccgcag ccgcccagac agatctgcag actggcccca   540

ttgcagagga ttagacacag ggtgcgtgga tcatagggtt tttgtacaga angcagtttt   600

aagaggaaat tggtcactgc atgtcatctc gaggggtggt gattcangga gccaggcctn   660

ggggttcana aagnacgttg ctngccatct tnggaggttt cctgctcact tntcaaangg   720

ncaggctngc cttttaaaaa tcaatgttcc ttccacccc aaaagggntt cttttttgcag   780

tgaatcanct nccaaaataa atagcccccn ttttttttgga aaagaacgtt tgnaaatccc   840

ncnttttaat ggnangtttt naattngggg gttnantcaa a   881

<210> 209
<211> 896
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(896)
<223> n is a, g, c or t

<400> 209
tttttccngg atnttnattt ntanacttat cccnccatt attttanggg ggnaanccct   60

nncanaatat tgtnttacaa atatcatttt ngtgtatgta tgtcaaaacc aaaactgcct   120

ttatgtcaat atgctgtaaa aatctatcag aatatatctt aattcttaac tttcattgtt   180

gtctgtgggt tgtcttgtat aattattatc acatctacag tattttctgt aggtaaatat   240

gaaatgtttt tttnatgtac caggggggaaa atgcccttta ataagccttt ccctagacaa   300

agcaccattt aggcgtttag aagcaagaac tagtganntc agaaattgct gtcatacata   360

ctcacctgtg aatggtcgta caaaggatcc caagcgcagg acttgtcctg gaagcagagg   420

atcggattcc accaggaaaa gaggcaagta gaaatgccaa atgccagcgc tccctttccc   480

cagctcatct tatttgtagg cactcagatt tttggaatcc tccaggacta acaaatanaa   540

accacactag gttgtttttc ctaattncct gtgaaatgag tcangtangt caaacanctt   600

atccactcca gagagagaac caattccttt gagctacact ccctgttttc cagtnaccct   660

aatnccctct ntggtgtccc ttgaanaaag ggnntgccna ccantgcatt ggagagccca   720

ccgggtttnt gaatgaagan nattgtnaaa antnnccaaa aagttaannn gccttcaagg   780

gganagtttn cctttntgaa nattnaagna ggaaaaatcc cannttaaaa tacctgggnt.   840

ccngttttttt nntaaaaaan cnnnnnactt ttctttggnc naangnttttt ttttttt   896

```
<210>   210
<211>   869
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(869)
<223>   n is a, g, c or t

<400>   210
nnccttctaa ttttntagtt tnnnagctca cttataaanc aggctacagt gttattctta      60

agtattcatt gttgtataac acactacccc caaaatttag gagcttaaaa taacagcaaa     120

cacttattat ctctcatggt tctgtgtgtt gactagacat ttcggctcct gtgcagatgg     180

ctggagcact gagctntttt ttnggtctac agtgctctcg cttacatagt aggcactagt     240

gttggctgct ggtagcaagc tcagttgggt gtgttgacca gannnnttgg ttctgctcta     300


gagcattgta atantgagca tttcaacagt attaacccaa catgcaaaca ctcactatag     420

taagcaaaat aaaataaaat aaagcccccc cccagatatc tatgctctaa aacttccaaa     480

cgtatgaata tgtnacctta aatagcaaaa ggcactntgc agtgtgattn angcaagatg     540

gggcagagtg tctgggaata tccangtgga acccaataat gcaaataaaa aaaatcnttt     600

tataanangg naggtaggaa ntaanacatc tgntcancat taccgctgcc nggttttttng    660

aaaaanaaaa ttnggaagaa aggggccnca agccaaggga atnccaggca tttcnctaan     720

tnggccaaaa caanannatn aaaantcntc ccccnnnnnc cnncnanaaa aaantgnaac     780

cctgggcgnc cncnttgatt tttnnnccca anganccbnc ctnaccaana nantnaaaaa     840

aaaatctntt gntcgnnttt nancnaaan                                       869



<210>   211
<211>   874
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(874)
<223>   n is a, g, c or t

<400>   211
tttttngggg atttcccttn tanantnnan ccccccccttt anttgggggg gaaatacnnc     60

ccattaacag ttttactcgc agcctctgct tngtctacat ctgctgccaa cttttaacta    120

atggcgagat actttcgcta tttccgatgc cattaggaaa caaatagaaa aatagtttgg    180
```

139

```
caacaacatc ttctcgaata ttatcacttg acaaattcta acgttttagg tggaaacgga      240

attttaannt tttgttttaa gaagcttaaa aaaaacaggc atgcttaatt agcataatgc      300

tgaatggcag ccaatcacaa actgaatttt taaagcnnga agtgtttgct cctggcgtgg      360

cgcgcccgcc tgtaatccgg gaatcccagc gttttgcgag cccacgccca ggccgaggag      420

ggaggatcct ttgttccacg agttcgacac cagcctaggc aatatagcag aattcagttc      480

aatgactcta ggctttagcc atgcagtatt aacaaatggg atattaacaa tattaacaaa      540

tgggataaaa accaagaact tgacaaatgt gttaatttcc tatttctgtt ttaatacatt      600

acacaaaact aactgcctga aaacaaaaca aaagntntta tttttatagt tctctaaatc      660

agaattttc attggggcnt aaaatcaagg tnntctgcaa ggctgcattc tttntgnagg      720

ctgtagggga naaatttcat tgtccttgnt ngnccttaa naaagcctgt tttnccttgg      780

cttggngncc ccttttttcaa ttcattttta aaaccccnan nnnatnngnn ccnntttctn      840

cctccncctc cncnttaaaa nattttttnt gngn                                 874
```

<210> 212
<211> 866
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(866)
<223> n is a, g, c or t

<400> 212
```
annnncnnnn nnnnnnnncc cccngatann ttgggggga aanncncnca tttgagtgnt       60

ncagggcaaa accaacagta aaccagacta ctaaagattt acttgtggaa ttttttttgca      120

aagtgtcaaa gggcttatag agaaatgaa acagttcttt aaagatgttc ttgagcgagg       180

ttttttttttt tttaacttac taaaagactt tatgttttag aacagttttt gtttacgttn      240

agcacgtagg acgtccccac tacacacaca gnttctctta ttaatagata ttagtatggt      300

acattngntg caactaatga accagtaatg ataaattatt aactaagatc catagntnat      360

tcctgcttcc tcacattnta tctaaagncc tttntctgnt ccaggatccc agctaggaga      420

tngaaagacc ccacctgnag gttnggcaag ctagctgagg atcgnnncgc atgatngaac      480

aagatggatn gcacgctggn tctccggccg ctngggngga gaggctatnc ggctatgact      540

gggcacaaca dacaancggc tgctctgatg ccgccgngnn ccggctgnca gcgcagggc       600

gcccggnncn tttnggnaan accgaccngn ccggngcccn gaangaacng caggacnagg      660

canngcggnn atcgnggntg gccacgacgg gcgnnccnng cgcannnggg cncnacgnng      720
```

```
nnacngaaac gggaagggna ccggcngnna nngggncaaa angccggggc aggaaccncn    780

grnaännaaa ccnggnnccn gccnnnaaang aaccanaaang ggngnnnnaa agnggngggn   840

ngnananccc ngnaaccggn nncccc                                         866
```

<210> 213
<211> 998
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(998)
<223> n is a, g, c or t

<400> 213
```
ttcggggggtc tanaangtnt nntnntncan nccccccccn tttttggggg gnaannncnn    60

nccagtttnn natttggnnn nggagcataa attnagtcgn ctctctcacc taaaactcat   120

ggtctggtgg aggctccgcc tcctttgtcc cctttcatgt ttctgtctca gcatgcctgg   180

ctccttaagg ntcttcatct tttgcaggtt tatctcaagn ctcaattgaa ccgccncctc   240

ctgncaggcn tttttnnnct gggaggtgag cagnngggtc cgggaatgtg ggagctaagg   300

gcatagatgt gaggaccncc ctatgaanag gaaaaggann cnnctggaat gcanacctgg   360

gactgtctgt atacctgcct ggtcactaaa tttctctgag aggcatcaac agnnaaaanc   420

ctganagggt tatngccaag agcatngatg gggtctgctt tctgggangc agggaataaa   480

ggnngtgata cccanaggga ttatntctca gccaggnccc tccttcccnt gtangannag   540

tcccttgagc cnccnmncna ctnancnntn ttttnaatna aacnccctn tnnncgggac    600

aacgggaann tccctatann cctcccannc tnggttgnnn aannccccggn gctaaaagca   660

atcnnncntn nccntnggtc tncacaaaan ggctnagaat naccangttg nagcccntn    720

ntncctant cccccctgna nnnctatnat ttnttccaan taaccaatna naccccccan    780

aacccannat acancacaac atngacccc ntcaaaacca acanccnnnt agacnttntn     840

ocnacntnnt aggncatnng cnaaccgnaa gcntttgttn tngaanctan ccaagggcct   900

cncnaacaan ttcaaaaana agtggtgntt cccccancct naaccccgng cccccacnnt   960

caacanannt aaaaannaan acccacnncc nntngtng                           998
```

<210> 214
<211> 956
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(956)
<223> n is a, g, c or t

<400> 214
tttttcggn ggattnctnn tttnnttnnt tnnccccc ngttnnttgg ggggaannc   60

cancgttctn nctatttcct tcttgacgag ttnttctgag cgggactctg gggttcnaaa   120

tgagctagcc cttaagtaac gccattttgc aaggcatgga aaaatacata actgagaata   180

gaaaagttca gatcgaggtc aggaacagat ggaacagggt cgaccggtcg accggtcgac   240

cctagagaac nntttntgt ttccagggtg ccccaaggac ctgaaatgac cctgtgcctt   300

atttgaacta accaatcagt tcgcttctcg cttctgttct ntcgcttctg ctccccgagc   360

tcaataaaag agcccacaac ccctcactcg gggcgccagt cctccgattg actgagtcgc   420

ccgggtaccc gtgtatccaa taaaccctct tgcagttgca tccgacttgt ggtctcgctg   480

ttccttggga gggtctcctc tgagtgattg actaccgtc agcgggggtc tttcaatctg   540

attgcctctt gcttgacggc aaggagtccc gaccactgaa cactgatgac ctcatctggt   600

gtgattgtct cttgcttgac ggcgaggagc cccgacgact gaacatggat agtcgccgcc   660

acagcacggt gatcanaagg ctttcgttcg acttatgant ccgacgntcc ggggagttca   720

aagccccttt tcnactccnt gggncctttt ngtnnttntc ttgnccacct ttcttgactt   840

cttnaanttt gcttctggan tgntaatncn natcnnaaan ccttgtttgn aaaancntgg   900

ccccnggncc cngnttcntt nacccccann tantgnttta ngnccnttt tggaaa   956

<210> 215
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(915)
<223> n is a, g, c or t

<400> 215
ccncaacctt ngagaccta aagacattgg agcagcccca tacacctcct cccagggcac   60

acaaaggccc ctgacatgcc catggcagtc caaggcctcc aattggagcc atctttggta   120

aatctggggc ccatcagccc ccactgccct tcctggtacc ctgagcatgc tggcaagggg   180

actnntttt gcatcccatc ttgtntcata tacccacagn acctgatgtg gacatgactc   240

accctggggt cctgtgagtc aataagggtg tntgantaag gggcagagca tttcaactta   300

gtcccataac ccatgagctc attaagcaaa tattacccat gcctagattt ggggccagtc   360

```
actacccact  ggaggctgtg  ggctccaagg  tatggcagca  ggggaggcca  gccaggcntc        420

tgcccagctc  acccttccct  gtgaggatgg  acnccagcca  ggcctcccac  ctccacccct        480

agactggggg  acccgggggtt  ggggggcaag  aaaggggacc  tgaaagtggn  tgtctnggag        540

ntaagcccat  ttncttnata  ctccnccaat  agggganccaa  gaaggngggt  tnagagttac        600

cccaanaact  caccccaacc  cantntnaac  gctgtggggt  ctcaangggg  acangcnaaa        660

acnaaaantn  anacnggccc  aaaaaagaac  aggtncggnc  ctnccccnan  ggacctttn        720

ttttctacca  ccttacccan  nanaatnctt  gaccaggggc  ntttccccaa  acncngnaaa        780

anctttcaag  cntngncact  ntnnanaccc  ngggcnnnnn  aaggnttagn  gcctcttnnn        840

ancnctntgn  cnggttncca  tngnntaaaa  accccaangn  aactcctcca  aanaacaagn        900

anccnntctn  ggttn                                                             915



<210>  216
<211>  949
<212>  DNA
<213>  Cercopithecus aethiops


<220>
<221>  misc_feature
<222>  (1)..(949)
<223>  n is a, g, c or t

<400>  216
tttncngngg  nanntttntg  nggaannctt  nncnnccccg  gntttttttgg  ggggnaannc        60

ncatcgttct  tactattgcc  ttcttgacga  gttnttctga  gcgggactct  ggggttcgaa        120

atgagctagc  ccttaagtaa  cgccattttg  caaggcatgg  aaaaatacat  aactgagaat        180

agaaaagttc  agatcgaggt  caggaacaga  tggnacaggg  tcgaccggtc  gaccggtcga        240

ccctagagaa  cctttntatg  tttccagggt  gccccaagga  cctgaaatga  ccctgtgcct        300

tatttgaact  aaccaatcnn  ttcgcttctc  gcttctgttc  ncgcgcttct  gctccccgag        360

ctcaataaaa  gagcccacaa  cccctcactc  ggggcgccag  tcctccgatt  gactgagtcg        420

cccgggtacc  cgtgtatcca  ataaaccctc  ttgcagttgc  atccgacttg  tggtctcgct        480

gttccttggg  agggtctcct  ctgagtgatt  gactacccga  gtggggaacg  ggggcagggc        540

gggtgggagg  agggcgcagg  aggctgagac  agcccaggtg  agagagggcc  aagcttgaaa        600

ggttttccca  ggcttgggga  gaggccctgg  tcaggatgtg  tatgggtaag  gggtgagaga        660

cagaggtncn  tggggcangc  ccggacctgt  ttttttngnc  cagtntcagt  tctgnttcnc        720

ttgnccctga  gaccccacgt  tcanagaggg  ttggnncggt  tgnggggnga  cnnttanccc        780

catctgatcc  catggtggnn  ntganganan  gggctaannc  nnancccntn  cagtcccttn        840
```

ttgcccncac tcgggcccn atcnnggnga agagggagnc cgctcgnccc nccccagga   900

agggnncngg nanaccggnn gnccccgnng caaccngnaa ccaacnnan   949

<210> 217
<211> 999
<212> DNA
<213> Cercopithecus aethiops

<220>   "
<221> misc_feature
<222> (1)..(999)
<223> n is a, g, c or t

<400> 217
ttttcccgng gannnnnntg nnnnttnnnn nttncccccc cocatnnnnc attgggggg   60

aaatnccccc catntaggcc tttnngcnaa agacccagtn ntctgcccct gggtncccnc   120

agganctctg caatggggaa gtgagccctc ctgaggcctg gctggcagga ggctcttcaa   180

ggtcatgtgg acttcccca acacctcgag tttctgcaca gcagccacgg agacgggcct   240

gggggctggc gggaaatttt tnnnaaggca atgtttncct gagtgggctg aaacctgaga   300

tgaggaaatg agaagacgtc aggtggctgg aggacacggg ctttaggaca gccagcaccc   360

agccctgtag ctgaggcctc cggagggagc cagagggaaa gggagtcccc tccccgcggc   420

ctgagtctct gccagtgccc agcactccca aaggatccac cccaacctga gagaccctaa   480

agacattgga gcagccccag acacctcctc ccagggccac aaaggcccct gacatgccca   540

tggcagtcca aggcctncaa ttggagccat cttttggtaa atctggggcc catcagcccc   600

cactgcncct tcctggtacc ctgagcatgc tggcaagggg actggaaact gcatcccatc   660

ttgtctcana tacccacagn acctgatgtg ggacatgact caccctgggg tcctgtgagt   720

caataagggt gtttgantaa ngggcagaac nnttnaactt antnccanaa acccatgagc   780

tcattaannc aaanttaccc tgcctanaat ngggggccant nactaccnac tggaaggttg   840

tggcttcang natggntnag ggaagnccnc nggctttccc aannnnncct tnccttngag   900

gnggacccac cagcctccan cnccccnna actgggaacc nngngnggca anaagggcng   960

aaanggtttt gantaaccna tttntanncc cnnggnaaa   999

<210> 218
<211> 962
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(962)

<223> n is a, g, c or t

<400> 218

```
nnncccggn actttcnnnt anngnanncc cccccctnat ttgggggna anncacannn       60

ttannnattt nnnnnngaca aagcttttt ccagggnntg aacngcngga tatttcctnn      120

ancaccatag ccgnctatgg gcttccaaat atccctttgc catttccaca agaactgcct     180

tatcgaaagg cttcttgaag ggaaagatgt aactctgnga gatgaatnct ccagaggaat     240

cctggatnnt nnccataggn angnctnaac ctgttcactc cngancttng ggagggtgca     300

cctggaagca agctctgggg tccctgggag agaaagcaca gcccctgccc tggagacact     360

caaagcctgg aagggaaggg cagnggggctg dacagagacc acaggtgtga cggtcctagg     420

tgggaggtgg gagctcagag ggggcaccta accccattgg gcagagtgct canggaaggc     480

tttgagtagc gccncagagg atgcngnaga ananccccag gaggagagcg acngnatgna     540

gagggaanag catttaccgn ngcctgggag tgngagaggg ctggcnggag aaaaaagagc     600

tccangaagc cacaaancct cannagnngc gtccacagcn cgatnctcna ncaccnacaa     660

cananccccg ccncatanaa agngcnccaa nccatcnntc acngaangaa nnaacaaaat     720

gaaanaaggg agatcaccna agggaganac gcngacaccc ccccnncccn accnganaac     780

cacnncanaa cntnnacccc gcanaccnaa ganccatgaa ganttnagca cggnanggcc     840

cannnaaaag ncataaanan aacngnagga aaagggaccg gacacccnan tnactacccc     900

cacnnntacc caaaaccaca ncnncngccn gggcgnaatn cccnacnacc aaccancccc     960
```

<210> 219
<211> 891
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(891)
<223> n is a, g, c or t

<400> 219

```
tttttngggg ntnnnnnggg gnnngnnnnt cccgcctnnc cttnggggn anncctnnnc       60

agttgggaat tnatttaaag aagggactta agggagatta ttaaagagcc agnaacgcaa     120

aggagagctg cggcaatcga caactaccga agacgcgaag cacattcacg aagcgttccc     180

ttcaatccgc acactacact cccacgaccc gcccttccg cccacagagc ccgccacttc      240

cgcctcanan ntnacgcccg ctctgtgctc ctaagggcct tcccgcggct gatcagacgc     300

cccgccccct agccgcaaca gaagccgtaa agctttctcc cgtcgcgatg cagcgctcaa     360
```

145

```
ggcgcctgcg cagaccctga aaagcggcca gggtggcccc gagcttccct tttccggttg      420

cagcgccgcg cggttaggtt ctctcgttct cgctcgcagc catgccgtcc aagggcccgc      480

tgcagtcggt gcaggtcttc ggacgcaagg tgagctagac gccagatggg aaggggaggg      540

gaaggagaag gtcagggtct gggagaggac ggtgggcagg aatacagggg gcaacatggg      600

agctggatcc cgagctcacg gggccacact ctcttgtatc ccacagaaga cagccacagc      660

tgtggcgcac tgcaaacgcg gcaatggtct catcaaggtg aacgggcggc cctggagat      720

gattgagccn cgcacgctnc aatacaaggt gnttggcatt gggncattcg ncgttgantt      780

ggattggagg acctntngga nataatagta gctnnttgaa agcttgaggg ggcnggntnt      840

cancanccgg gnttttnana anttngnttn gtntnnnnaa aaggggttt t                891
```

```
<210>   220
<211>   902
<212>   DNA
<213>   Cercopithecus aethiops


<220>
<221>   misc_feature
<222>   (1)..(902)
<223>   n is a, g, c or t

<400>   220
tttttnnngg nntataattt ganntatnta tcccncccat aaaccttggg ggggaanaca      60

aggnctnaag ttttttagga ttgtgctact gtactccagg gtgagtgaca gcaagtatac      120

tgttcttaaa aaaagaacct tatatattaa aaaaaaattt ttttttaact gaccctgcaa      180

tgcacatatg cttccttta aaagtagtaa acttcagaag gggcagaaat cagactctgg       240

tttctttcca ttttnagcca aagaaactga nagtnccaaa cagggaacag aagaaccct      300

ttcacaagca agcatttaaa cagacccaaa ttcggccgcg cggctcacca ggctggtcag      360

gagttctaga ccagcctggc cgacatggtg aaaccacgtc tctcctgaaa atacaaacat      420

tagccggccg tggtggtgtg cgcctatagt cccagccacc cgggaggctg aggcaagaga      480

attgcttgaa cccggagggt ggaggttgca gcgatccgag atcgtgccac tgcactctcc      540

agcctgggcg acagagcgag actccctctc aaacaaataa atngaaaaaa aaataaacag      600

acccaaattc aagctatttc aatacttact gagcacttac aatgtctaaa acgctgcttt      660

tagacgcctt ggggtttnt taaggatnaa aacacttgnt ncttngtgaa aatnaaanct      720

atgaaaactg ggtgttcctt caanccttn gggntccccc ccggnttccc cnnttnaaat      780

gaaccttnct aaacattncc aatttnaaa agncanccc nttaattntt taanacnccc      840

ccaatttnaa nnttttaaan ttttntnaa acnntaäanc cccgggtttt ttttnncnaa      900
```

aa

902

<210> 221
<211> 907
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(907)
<223> n is a, g, c or t

<400> 221

```
ccncannggt agntccgctc gccttccgcc ttgtaagcng gaaaggtgct tcgcgaggtc      60

tcgccttcgg ggtccgacat ggtgaccgga tttagagacg ctaaagcaga gacaatcgaa     120

gaaaagctgg agaacctcta tctggttctg gtttgtggaa gctccgtctc ttagcaaccg     180

cgagacgann ttttcagcga tttccggttc cgtccctgtc tggcaagggc ccggattctg     240

ggtgcaacct gccggcgtgc gcgtgcgcca gttctntnnn gcaccgggcc ggagagtgat     300

gagtgcgtgg ctggcggctg agctccttag tgtttgctgt tgcacgctcc ttcggttctc     360

tctggagtta ctgcgtgaaa aggctgcctt gtaagacagc caagaaaaca ggaagagggt     420

tggaggcaaa gttccnaata gggattgaaa gaccccacct gtnggttttg gcaagctagc     480

tgaggatcgt tcgcatgatt gaacaagatg gattgcacgc tggtttcttc ggccgcttgg     540

gtggagaggc tatttcggct atgactgggc acacagacat tcggctnctt ttantgccnc     600

cngngtncng gctgtnagcg naggggacgn cccgggttct ttnttgnaaa gacccnaccg     660

ttccggtgcc cttaatnaan ctgnanggac gagnnnancc cngntttatt ttgntgggcn     720

ncaacggncn ttccttnnac anctngntcn ncancnttgt nanttaaccn gnaanggnnc     780

tngntngttt tggncnaaat annccgggca aggaactccn nnnnannccc ccgtgtnnnt     840

ncccacaaan tatcnattng ggtancnaan cngggnnnnn tnaccnnnac ccgnnnnccg     900

ccnanct                                                               907
```


<210> 222
<211> 955
<212> DNA
<213> Cercopithecus aethiops

<220>
<221> misc_feature
<222> (1)..(955)
<223> n is a, g, c or t

<400> 222
```
tttttccggg ggaannnnnn nnggnnnnaa nnnnntcccc ncccatnnn ccttnggggg       60
```

147

```
gnaanaccccc nnncaattcc ctatttggna actttgcctc caaccctctt cctgttttct      120

tggctgtctt acaaggcagc cttttcacgc agtaactcca gagagaaccg aaggagcgtg      180

caacagcaaa cactaaggag ctcagccgcc agccacgcac tcatcactct ccggcccggt      240

gcgcggcaga actggcgcac nnttnnnccg gcaggttgca cccagaatcc gggcccttgc      300

cagacaggga cggaaccgga aatcgctgta cgtctcgtct cacggttgct aagagacgga      360

gcttccacaa accagaacca gatagaggtt ctccagcttt tcttcgattg tctctgcttt      420

agcgtctcta aatccggtca ccatgtcgga ccccgaaggc gagacctcgc gaagcacctt      480

tccctcttac atggcggaag gcgagcggct ctacctgtgc ggagaattct gtgtgaaatt      540

gttatccgct cacaattccc acacaacatg agcgtcagac cccgaagaaa agatcaaagg      600

atcttctttg agatcccttt ttttctgcgc gtaatctgct gcttgcaaac aaaaaaacca      660

ccgntaccag cggnggtttt gnttngccgg atcaagagnt accaaantnt tttttcnnaa      720

gnaacttggc ttnagcanaa cccnaanacc aaatactgnc ntttngngta cccgtantta      780

ggcccccccct taaaaanttn nnanccncta atanccngtt ttntaatttn ttacaanggg      840

tnttgcnagg gnaaaaattn gttttaccgg ttgnctnaaa aaaattttcc gaaaggcccn      900

ngtnngntaa aggggntctg cccaacccat tgggnnannt ccncccannt naatc          955
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<210>  223
<211>  927
<212>  DNA
<213>  Cercopithecus aethiops


<220>
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<222>  (1)..(927)
<223>  n is a, g, c or t

<400>  223
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cntatcatnn cccatcactg ggtaatattc acagnatcaa attatcctcc ctaacccagt      120

cctgtgaata ttctcattga tcctcaaact cactttggcc tcagtgatcc ccaacagcct      180

cctttacaac cttacaacat ccaagttcct gttctgtgag agtttcctct cgaaacacaa      240

cattccgtac aattcagtct ctcactccgt caatcctcta cattggcagt gagaccttat      300

tttgtgaccc tttactttac agcagccatt tcaaagagac attctctagc ctgaaagggc      360

tccagattct ttcaactttc tattatgtat gcattgccaa tattgaattt gcactatctt      420

atcaactatt ctaaaactac tgacatttgc agaaactggt catttgttct tagggaaaat      480

gtctgtgtta tccaaaaatg gagattaaaa acttgcacac attcctactt gatttccaca      540
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gngacctgat ctatggtatc tagcntcctt cccctctgcc ccaagttcac atttccatca    600

gctcatatat actcttccct ttctactcct gctgacaggg tccaaggata ctgcctcaaa    660

aactctataa aaganaataa aaactnatta actggctttn ctatcnaaaa nctttcnact    720

agnaatatta anaaangntt ttcaaccggt nggatccgaa ancatccnaa gnagggntna    780

ngccnaaaaa aaaaataatn nntttccccn aaaaannaaa aaatagnntn tnanggggggc    840

ccngnncntn gnaaaagaaa naannccggn cntnnaaana nnannaaaaa nntccncngg    900

nttnannnnn aaaaancatn aancnnn                                        927
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<210>  224
<211>  936
<212>  DNA
<213>  Cercopithecus aethiops


<220>
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<222>  (1)..(936)
<223>  n is a, g, c or t

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cccccacag nnccacttcg cggctgccag gcagtcaggc aaagnaggcc gaagcaaagc     120

cctagaagca aagccacagg aataagtcag ctttcccaga ggtcaaagaa ggctgtaggg     180

ccacctgcca cgcctcccga ccccggccgc gcggcctggg cccgctcccc aaccaaagag     240

gcccgaattc agagannttt tagcagtttc acagaaagct tctttccagt tttgaacgga     300

agatatttcc ttttcaccg taggcctcta tgggcttcca aatatccctt tgccaattcc     360

acaagaacag ccttagcgaa aggcttcttg aagggaaaga tgtaactctg tgaaatgaat     420

tctgcttata ggtcttgaga taaagtcacc gatctcatat catggattat aaggttttcc     480

ttctattttc tggcattttg gatatgtaat gatgagcatc agaaagttta atcatattta     540

atttttagaa ttattaaata ctcctgaggt cattttggtt gattttgngt ggctttcaac     600

cataaagaga tcaatgcctt gcagatataa agcttccctt ttccttcttt aataattnta     660

aactctgaat tnatgnctac agatatntaa tngatcataa atganaaatg ngatactatt     720

cnctacctcc ttatctgttc tcggaanaga ctatacancc ctgcaannat ngaagttnan     780

gattgcttnt acgaaannna aaaaaaattn acttnttttt nggcaanana aaatgcttcc     840

tccgttgnna actcccctca nggngtntta gggggnannc taccttnaan ttccntngnc     900

ctggnnncng tnnnaggnan tgcaaanngn tttctt                              936
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<210>   225
<211>   605
<212>   DNA
<213>   Cercopithecus aethiops

<220>
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<222>   (1)..(605)
<223>   n is a, g, c or t

<400>   225
ttttnccnng nnntacnnct tnnnnanttn annccccccc attattttng gggggaaacc   60

tagnaaaaat aatantgtac aagattttat ttttgtcttt aaccagaatg atgtatttgg   120

ttaagaagat agtccaagtt aaaggcatac attcaagcta gtggcacatt cggaagagca   180

gacaaagata gttggttgca aatgggaaat ttaagccatg atcttaaaag gacagaatgg   240

atatttgtta cttttnctat gggaataatt gatttttttc accttccctt tcttggattt   300

ttttttttt ttaaattagt ttggttactt taaccttact gtcggttata ttggttctct   360

ttttatgtct gagttttttt ttttttttga dacggagtct tgctctgtcg cccaggctgg . 420

agtgcagtgg ccggatctca gctcactgca agctctgcct cccgggttta caccattctc   480

ctgcctcagc ctnctgagta gctaggacta caggcgcccg ccacctngcc cggctagttt   540

tttgtatttt ttagtagaga cgggtttnna cccnnntnnn ncanatggtt tnnntctnct   600

ntcct   605

<210>   226
<211>   654
<212>   DNA
<213>   Cercopithecus aethiops

<220>
<221>   misc_feature
<222>   (1)..(654)
<223>   n is a, g, c or t

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tttntngggg nnnnnnnngn attgnnnntc cccccgtnn nttgggggn aanncnncc   60

antactgttt gaggaaagac tgaggntcag atggcagagg ctccntagag gaaggaggct   120

acagccttga gggcatcagc ttcccacact cccaacctgc tgcctctctc tgctggaatg   180

aggaggggcc tcctggctgg gggtctccag ggtggaggga ggagctcaca ttcttagcat   240

tcctnttncc ctgagttgca aggaagacct ggtgagcatg ctgaccccag aggagtgact   300

caggcccatg gctcgagtgc ctgaggaggg accagggtcg gggatggggc atgagtcagc   360

ctggcaggtc ccataagaag ggaagggaag ggagagaaat gggggctgca caggtgtgag   420

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ggtctgtgca tgtctgtgtg gtgtggtggg gtgtctggat atccgngtgt tctggatctg    480

agtgttagtg tatccgncag cacaacctct gtgtgagggt gtgtctnggc gagggtgggc    540

ttctgtggat gtcccntgtg tggnatgtgt gngtgtgtgt gtgngngact aanntatnnc    600

cttcaacnng ggntctnncc caangngnnt ntggatctnc atannatgtc tctc          654
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<210>    227
<211>    2635
<212>    DNA
<213>    homo sapiens


<220>
<221>    CDS
<222>    (285)..(1679)

<400>    227
ggccgacgcg agcgccgcgc ttcgcttcag ctgctagctg gccaaggga ggcgaccgcg      60

gagggtggcg aggggcggcc aggacccgca gccccggggc cgggccggtc cggaccgcca    120

gggagggcag gtcagtgggc agatcgcgtc cgcgggattc aatctctgcc cgctctgata    180

acagtccttt tccctggcgc tcacttcgtg cctggcaccc ggctgggcgc ctcaagaccg    240

ttgtctcttc gatcgcttct ttggacttgg cgaccatttc agag atg tct tcc aga     296
                                                   Met Ser Ser Arg
                                                   1

agt acc aaa gat tta att aaa agt aag tgg gga tcg aag cct agt aac     344
Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys Pro Ser Asn
5                   10                  15                  20

tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa att gca cac     392
Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu Ile Ala His
                25                  30                  35

tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga aag ctg act     440
Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly Lys Leu Thr
                40                  45                  50

gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc ctt gag gct     488
Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val Leu Glu Ala
            55                  60                  65

gag aag gag aag aat gct tat caa ctc aca gag aag gac aaa gaa ata     536
Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp Lys Glu Ile
            70                  75                  80

cag cga ctg aga gac caa ctg aag gcc aga tat agt act acc gca ttg     584
Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr Thr Ala Leu
85                  90                  95                  100

ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg agg gag cag     632
Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg Arg Glu Gln
                105                 110                 115

gtg ttg aaa gcc tta tct gaa gag aga gac gta ttg aaa caa cag ttg     680
```

```
Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys Gln Gln Leu
         120                 125             130

tct gct gca acc tca cga att gct gaa ctt gaa agc aaa acc aat aca       728
Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys Thr Asn Thr
         135                 140                 145

ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac tca tca ata       776
Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn Ser Ser Ile
         150                 155                 160

aat aat att cat gaa atg gaa ata cag ctg aaa gat gct ctg gag aaa       824
Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala Leu Glu Lys
165                 170                 175                 180

aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc tat gta aaa       872
Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val Tyr Val Lys
                 185                 190                 195

gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg gaa aca gct       920
Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr Glu Thr Ala
             200                 205                 210

gct cat tca ctc cca cag cag aca aaa aag cct gaa tca gaa ggt tat       968
Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser Glu Gly Tyr
             215                 220                 225

ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg gca agt gca      1016
Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu Ala Ser Ala
         230                 235                 240

aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag ctg agt ttt      1064
Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln Leu Ser Phe
245                 250                 255                 260

gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa aaa gaa gtt      1112
Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln Lys Glu Val
                 265                 270                 275

cac aat tta aat cag ctg ttg tat tca caa aga agg gca gat gtg caa      1160
His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala Asp Val Gln
             280                 285                 290

cat ctg gaa gat gat agg cat aaa aca gag aag ata caa aaa ctc agg      1208
His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln Lys Leu Arg
         295                 300                 305

gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag aag aag aga      1256
Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu Lys Lys Arg
         310                 315                 320

tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca tct ctg cta      1304
Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr Ser Leu Leu
325                 330                 335                 340

aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa caa cag atg      1352
Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu Gln Gln Met
                 345                 350                 355

cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac cgt caa cat      1400
Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp Arg Gln His
```

```
              360                365                370

gtg cag cat caa ttg ctt gta att ctt aag gag ctc cga aaa gca aga   1448
Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu Arg Lys Ala Arg
            375                380                385

aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat gag ttt gcc   1496
Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His Glu Phe Ala
    390                395                400

atc aca gag cca tta gtc act ttc caa gga gag act gaa aac aga gaa   1544
Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu Asn Arg Glu
405                410                415                420

aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc aat gaa agc   1592
Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu Asn Glu Ser
                425                430                435

ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc act gag cat   1640
Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His
                440                445                450

cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag caaaataagt   1689
Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
                455                460

atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg ggcattttga   1749

attatatatt tcacattttg cataaaactg cctatctacc tttgacactc cagcatgcta   1809

gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac ctccctgaca   1869

tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg agactactaa   1929

cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt gctaatgggt   1989

taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca aagataatta   2049

accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac ctacaatcct   2109

aattttgatg tccattgtta agaggtggtg atagatacta tttttttttt catattgtat   2169

agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac cattgaaact   2229

taacccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt ttgaggcata   2289

atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac tgtaacttga   2349

attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat aaaccatgt   2409

agccctctca tttgattgac agtattttag ttattttgg cattcttaaa gctgggcaat   2469

gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt ttgtaaacca   2529

aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac tgtaaatgag   2589

aaaagaataa aattatttaa tgtttaaaa aaaaaaaaaa aaaaaa                   2635
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<210>   228
<211>   464

<212>   PRT
<213>   homo sapiens

<400>   228

Met Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser
1   5   10   15

Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
                20   25   30

Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
            35   40   45

Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
    50   55   60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65   70   75   80

Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
                85   90   95

Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
                100   105   110

Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
            115   120   125

Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
    130   135   140

Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145   150   155   160

Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
                165   170   175

Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
            180   185   190

Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
    195   200   205

Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
    210   215   220

154

```
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225                 230                 235                 240

Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
                245                 250                 255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
                260                 265                 270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
            275                 280                 285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
        290                 295                 300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
    305                 310                 315                 320

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
                325                 330                 335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
            340                 345                 350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
        355                 360                 365

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu
    370                 375                 380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385                 390                 395                 400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
            405                 410                 415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
        420                 425                 430

Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
        435                 440                 445

Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
    450                 455                 460


<210>  229
<211>  2635
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<212>   DNA
<213>   homo sapiens


<220>
<221>   CDS
<222>   (285)..(1679)

<400>   229
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gagggtggcg aggggcggcc aggacccgca gccccggggc cgggccggtc cggaccgcca     120

gggagggcag gtcagtgggc agatcgcgtc cgcgggattc aatctctgcc cgctctgata     180

acagtccttt tccctggcgc tcacttcgtg cctggcaccc ggctgggcgc ctcaagaccg     240

ttgtctcttc gatcgcttct ttggacttgg cgaccatttc agag atg tct tcc aga      296
                                                  Met Ser Ser Arg
                                                  1


agt acc aaa gat tta att aaa agt aag tgg gga tcg aag cct agt aac      344
Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys Pro Ser Asn
5                10                  15                  20


tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa att gca cac      392
Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu Ile Ala His
                25                  30                  35


tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga aag ctg act      440
Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly Lys Leu Thr
                40                  45                  50


gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc ctt gag gct      488
Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val Leu Glu Ala
            55                  60                  65


gag aag gag aag aat gct tat caa ctc aca gag aag gac aaa gaa ata      536
Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp Lys Glu Ile
            70                  75                  80


cag cga ctg aga gac caa ctg aag gcc aga tat agt act acc gca ttg      584
Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr Thr Ala Leu
85                  90                  95                  100


ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg agg gag cag      632
Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg Arg Glu Gln
                105                 110                 115


gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa caa cag ttg      680
Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys Gln Gln Leu
                120                 125                 130


tct gct gca acc tca cga att gct gaa ctt gaa agc aaa acc aat aca      728
Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys Thr Asn Thr
                135                 140                 145


ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac tca tca ata      776
Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn Ser Ser Ile
            150                 155                 160
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156

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aat aat att cat gaa atg gaa ata cag ctg aaa gat gct ctg gag aaa      824
Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala Leu Glu Lys
165             170             175                 180

aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc tat gta aaa      872
Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val Tyr Val Lys
                185             190                 195

gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg gaa aca gct      920
Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr Glu Thr Ala
                200             205                 210

gct cat tca ctc cca cag cag aca aaa aag cct gaa tca gaa ggt tat      968
Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser Glu Gly Tyr
                215             220                 225

ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg gca agt gca     1016
Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu Ala Ser Ala
230             235             240

aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag ctg agt ttt     1064
Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln Leu Ser Phe
245             250             255                 260

gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa aaa gaa gtt     1112
Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln Lys Glu Val
                265             270                 275

cac aat tta aat cag ctg ttg tat tca caa aga agg gca gat gtg caa     1160
His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala Asp Val Gln
                280             285                 290

cat ctg gaa gat gat agg cat aaa aca gag aag ata caa aaa ctc agg     1208
His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln Lys Leu Arg
                295             300                 305

gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag aag aag aga     1256
Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu Lys Lys Arg
310             315             320

tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca tct ctg cta     1304
Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr Ser Leu Leu
325             330             335                 340

aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa caa cag atg     1352
Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu Gln Gln Met
            345             350                 355

cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac cgt caa cat     1400
Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp Arg Gln His
                360             365                 370

gtg cag cat caa ttg ctt gta att ctt aag gag ctc cga aaa gca aga     1448
Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu Arg Lys Ala Arg
                375             380                 385

aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat gag ttt gcc     1496
Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His Glu Phe Ala
390             395             400

atc aca gag cca tta gtc act ttc caa gga gag act gaa aac aga gaa     1544
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    Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu Asn Arg Glu
    405             410             415             420

    aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc aat gaa agc       1592
    Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu Asn Glu Ser
                    425             430             435

    ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc act gag cat       1640
    Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala Thr Glu His
                440             445             450

    cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag caaaataagt        1689
    Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
                455             460
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    atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg ggcattttga    1749

    attatatatt tcacattttg cataaaactg cctatctacc tttgacactc cagcatgcta    1809

    gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac ctccctgaca    1869

    tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg agactactaa    1929

    cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt gctaatgggt    1989

    taatgcacca gcaagcaaaa tatttatgt tttggggggtt tgaaaaatca aagataatta    2049

    accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac ctacaatcct    2109

    aattttgatg tccattgtta agaggtggtg atagatacta ttttttttttt catattgtat   2169

    agcggttatt agaaaagttg gggattttct tgatctttat tgctgcttac cattgaaact    2229

    taacccagct gtgttcccca actctgttct gcgcacgaaa cagtatctgt ttgaggcata    2289

    atcttaagtg gccacacaca atgttttctc ttatgttatc tggcagtaac tgtaacttga    2349

    attacattag cacattctgc ttagctaaaa ttgttaaaat aaactttaat aaacccatgt    2409

    agccctctca tttgattgac agtattttag ttatttttgg cattcttaaa gctgggcaat    2469

    gtaatgatca gatctttgtt tgtctgaaca ggtattttta tacatgcttt ttgtaaacca    2529

    aaaacttttta aatttcttca ggttttctaa catgcttacc actgggctac tgtaaatgag   2589

    aaaagaataa aattatttaa tgttttaaaa aaaaaaaaaa aaaaaa                    2635
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    1               5               10              15

    Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
                20              25              30
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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
        35   40   45

Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
        50   55   60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65   70   75   80

Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
                85   90   95

Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
            100   105   110

Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
        115   120   125

Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
    130   135   140

Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145   150   155   160

Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
            165   170   175

Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
        180   185   190

Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
        195   200   205

Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
    210   215   220

Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225   230   235   240

Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
            245   250   255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
            260   265   270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
        275   280   285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
    290   295   300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
305   310   315   320

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
            325   330   335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
        340   345   350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
        355   360   365

Asp Arg Gln His Val Gln His Gln Leu Leu Val Ile Leu Lys Glu Leu
    370   375   380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385   390   395   400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
                405   410   415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
            420   425   430

Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
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Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
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                                Met Leu Arg Val Ile Val Glu Ser
                                 1               5

gcc agc aat atc cct aaa acg aaa ttt ggc aag ccg gat cct att gtt      160
Ala Ser Asn Ile Pro Lys Thr Lys Phe Gly Lys Pro Asp Pro Ile Val
     10              15              20

tct gtc att ttt aag gat gag aaa aag aaa aca aag aaa gtt gat aat      208
Ser Val Ile Phe Lys Asp Glu Lys Lys Lys Thr Lys Lys Val Asp Asn
25              30              35              40

gaa ttg aac cct gtc tgg aat gag att ttg gag ttt gac ttg agg ggt      256
Glu Leu Asn Pro Val Trp Asn Glu Ile Leu Glu Phe Asp Leu Arg Gly
                 45              50              55

ata cca ctg gac ttt tca tct tcc ctt ggg att att gtg aaa gat ttt      304
Ile Pro Leu Asp Phe Ser Ser Ser Leu Gly Ile Ile Val Lys Asp Phe
             60              65              70

gag aca att gga caa aat aaa tta att ggc acg gcg act gta gcc ctg      352
Glu Thr Ile Gly Gln Asn Lys Leu Ile Gly Thr Ala Thr Val Ala Leu
         75              80              85

aag gac ctg act ggt gac cag agc aga tcc ctg ccg tac aag ctg atc      400
Lys Asp Leu Thr Gly Asp Gln Ser Arg Ser Leu Pro Tyr Lys Leu Ile
         90              95                 100

tcc ctg cta aat gaa aaa ggg caa gat act ggg gcc acc att gac ttg      448
Ser Leu Leu Asn Glu Lys Gly Gln Asp Thr Gly Ala Thr Ile Asp Leu
105             110             115             120

gtg atc ggc tat gat ccg cct tct gct cca cat cca aat gac ctg agc      496
Val Ile Gly Tyr Asp Pro Pro Ser Ala Pro His Pro Asn Asp Leu Ser
             125             130             135

ggg ccc agc gtg cca ggc atg gga gga gat ggg gaa gaa gat gaa ggt      544
Gly Pro Ser Val Pro Gly Met Gly Gly Asp Gly Glu Glu Asp Glu Gly
             140             145             150

gat gaa gac agg ttg gac aat gca gtc agg ggc cct ggg ccc aag ggg      592
Asp Glu Asp Arg Leu Asp Asn Ala Val Arg Gly Pro Gly Pro Lys Gly
             155             160             165

cca gtt ggg acg gtg tcg gaa gct cag ctt gct cgg agg ctc acc aaa      640
Pro Val Gly Thr Val Ser Glu Ala Gln Leu Ala Arg Arg Leu Thr Lys
         170             175             180

gta aag aac agc cgg cgg atg ctg tca aat aag cca cag gac ttc cag      688
Val Lys Asn Ser Arg Arg Met Leu Ser Asn Lys Pro Gln Asp Phe Gln
185             190             195             200

atc cgc gtc cga gtg att gag ggc cga cag tta agt ggt aac aac ata      736
Ile Arg Val Arg Val Ile Glu Gly Arg Gln Leu Ser Gly Asn Asn Ile
             205             210             215

agg cct gtg gtc aaa gtt cac gtc tgt ggc cag aca cac cga aca aga      784
Arg Pro Val Val Lys Val His Val Cys Gly Gln Thr His Arg Thr Arg
             220             225             230

atc aag aga gga aac aac cct ttt ttt gat gag ttg ttt ttc tac aat      832
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161

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               Ile Lys Arg Gly Asn Asn Pro Phe Phe Asp Glu Leu Phe Phe Tyr Asn
                       235                 240                 245

gtc aac atg acc cct tct gaa ttg atg gat gag atc atc agc atc cgg          880
Val Asn Met Thr Pro Ser Glu Leu Met Asp Glu Ile Ile Ser Ile Arg
        250                 255                 260

gtt tat aat tct cac tct ctg cgg gca gat tgt ctg atg ggg gaa ttt          928
Val Tyr Asn Ser His Ser Leu Arg Ala Asp Cys Leu Met Gly Glu Phe
265                 270                 275                 280

aag att gat gtt gga ttt gtt tat gat gaa cct ggc cat gct gtc atg          976
Lys Ile Asp Val Gly Phe Val Tyr Asp Glu Pro Gly His Ala Val Met
                285                 290                 295

aga aag tgg ctt ctt ctc aat gac ccg gaa gat acc agt tca ggt tct          1024
Arg Lys Trp Leu Leu Leu Asn Asp Pro Glu Asp Thr Ser Ser Gly Ser
                300                 305                 310

aaa ggt tat atg aaa gtc agc atg ttt gtc ctg gga acc gga gat gag          1072
Lys Gly Tyr Met Lys Val Ser Met Phe Val Leu Gly Thr Gly Asp Glu
                315                 320                 325

cct cct cct gag aga cga gat cgt gat aat gac agt gat gat gtg gag          1120
Pro Pro Pro Glu Arg Arg Asp Arg Asp Asn Asp Ser Asp Asp Val Glu
        330                 335                 340

agt aat ttg tta ctc cct gct ggc att gcc ctc cgg tgg gtg acc ttc          1168
Ser Asn Leu Leu Leu Pro Ala Gly Ile Ala Leu Arg Trp Val Thr Phe
345                 350                 355                 360

ttg ctg aaa atc tac cga gct gag gac atc ccc cag atg gat gat gcc          1216
Leu Leu Lys Ile Tyr Arg Ala Glu Asp Ile Pro Gln Met Asp Asp Ala
                365                 370                 375

ttc tca cag aca gta aag gaa ata ttt gga ggc aat gca gat aag aaa          1264
Phe Ser Gln Thr Val Lys Glu Ile Phe Gly Gly Asn Ala Asp Lys Lys
                380                 385                 390

aat ctc gtg gat cct ttt gta gaa gtt tcc ttt gct gga aaa aag gtt          1312
Asn Leu Val Asp Pro Phe Val Glu Val Ser Phe Ala Gly Lys Lys Val
                395                 400                 405

tgt aca aac ata att gag aaa aat gca aac cca gag tgg aat cag gtc          1360
Cys Thr Asn Ile Ile Glu Lys Asn Ala Asn Pro Glu Trp Asn Gln Val
        410                 415                 420

gtc aat ctt cag atc aag ttt cct tca gtg tgt gaa aaa ata aaa cta          1408
Val Asn Leu Gln Ile Lys Phe Pro Ser Val Cys Glu Lys Ile Lys Leu
425                 430                 435                 440

aca ata tat gac tgg gac cgt ctt act aaa aat gat gta gtt gga aca          1456
Thr Ile Tyr Asp Trp Asp Arg Leu Thr Lys Asn Asp Val Val Gly Thr
                445                 450                 455

aca tat cta cac ctc tct aaa att gct gcc tct ggt ggg gaa gtg gaa          1504
Thr Tyr Leu His Leu Ser Lys Ile Ala Ala Ser Gly Gly Glu Val Glu
                460                 465                 470

gat ttc tca tct tcg gga act ggg gct gca tca tat aca gta aac aca          1552
Asp Phe Ser Ser Ser Gly Thr Gly Ala Ala Ser Tyr Thr Val Asn Thr
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162

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                475                    480                    485

    gga gaa aca gag gta ggc ttt gtt cca acg ttt gga cct tgt tac ctg    1600
    Gly Glu Thr Glu Val Gly Phe Val Pro Thr Phe Gly Pro Cys Tyr Leu
        490                    495                    500

    aat ctt tat gga agc ccc agg gag tac acg gga ttc cca gac ccc tat    1648
    Asn Leu Tyr Gly Ser Pro Arg Glu Tyr Thr Gly Phe Pro Asp Pro Tyr
    505                    510                    515                    520

    gat gag ctg aat act gga aag ggg gaa gga gtt gcc tac aga ggc agg    1696
    Asp Glu Leu Asn Thr Gly Lys Gly Glu Gly Val Ala Tyr Arg Gly Arg
                    525                    530                    535

    atc ttg gtt gaa tta gcc act ttt ctt gag aag aca cca cca gat aaa    1744
    Ile Leu Val Glu Leu Ala Thr Phe Leu Glu Lys Thr Pro Pro Asp Lys
                    540                    545                    550

    aag ctt gag ccc att tca aat gat gac ctg ctg gtt gtt gag aaa tac    1792
    Lys Leu Glu Pro Ile Ser Asn Asp Asp Leu Leu Val Val Glu Lys Tyr
                    555                    560                    565

    cag cga agg cgg aag tac agc ctg tct gcc gtg ttt cat tca gcc acc    1840
    Gln Arg Arg Arg Lys Tyr Ser Leu Ser Ala Val Phe His Ser Ala Thr
        570                    575                    580

    atg ttg caa gat gtt ggt gag gcc att cag ttt gaa gtc agc att ggg    1888
    Met Leu Gln Asp Val Gly Glu Ala Ile Gln Phe Glu Val Ser Ile Gly
    585                    590                    595                    600

    aac tat ggc aac aag ttt gac acc acc tgt aag cct ttg gca tca aca    1936
    Asn Tyr Gly Asn Lys Phe Asp Thr Thr Cys Lys Pro Leu Ala Ser Thr
                    605                    610                    615

    act cag tac agc cgt gct gta ttt gat ggc aac tac tat tat tac ttg    1984
    Thr Gln Tyr Ser Arg Ala Val Phe Asp Gly Asn Tyr Tyr Tyr Tyr Leu
                620                    625                    630

    cct tgg gcc cac acc aag cca gtt gtt acc ctg act tca tac tgg gag    2032
    Pro Trp Ala His Thr Lys Pro Val Val Thr Leu Thr Ser Tyr Trp Glu
                635                    640                    645

    gat att agt cat cgc ctg gat gcg gtg aac act ctc cta gct atg gca    2080
    Asp Ile Ser His Arg Leu Asp Ala Val Asn Thr Leu Leu Ala Met Ala
                650                    655                    660

    gaa cgg ctg caa aca aat ata gaa gct cta aaa tca ggg ata caa ggt    2128
    Glu Arg Leu Gln Thr Asn Ile Glu Ala Leu Lys Ser Gly Ile Gln Gly
    665                    670                    675                    680

    aaa att cct gca aac cag ctg gct gaa ttg tgg ctg aag ctg ata gat    2176
    Lys Ile Pro Ala Asn Gln Leu Ala Glu Leu Trp Leu Lys Leu Ile Asp
                    685                    690                    695

    gaa gtt ata gaa gac acg aga tac acg ttg cct ctc aca gaa gga aaa    2224
    Glu Val Ile Glu Asp Thr Arg Tyr Thr Leu Pro Leu Thr Glu Gly Lys
                    700                    705                    710

    gcc aac gtc aca gtt ctc gat act cag atc cga aag ctg cgg tcc agg    2272
    Ala Asn Val Thr Val Leu Asp Thr Gln Ile Arg Lys Leu Arg Ser Arg
                    715                    720                    725
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163

tct ctc tcc caa ata cat gag gcg gct gtg agg atg agg tcg gaa gcc   2320
Ser Leu Ser Gln Ile His Glu Ala Ala Val Arg Met Arg Ser Glu Ala
        730   735   740

aca gat gtg aag tcc aca ctg gca gaa att gag gac tgg ctt gat aaa   2368
Thr Asp Val Lys Ser Thr Leu Ala Glu Ile Glu Asp Trp Leu Asp Lys
745   750   755   760

tta atg cag ctg act gaa gag cca cag aac agc atg cct gac atc atc   2416
Leu Met Gln Leu Thr Glu Glu Pro Gln Asn Ser Met Pro Asp Ile Ile
              765   770   775

atc tgg atg atc cgg gga gag aag aga ctg gcc tat gca cga att ccc   2464
Ile Trp Met Ile Arg Gly Glu Lys Arg Leu Ala Tyr Ala Arg Ile Pro
              780   785   790

gca cat cag gtc ttg tac tcc acc agt ggt gag aat gca tct gga aaa   2512
Ala His Gln Val Leu Tyr Ser Thr Ser Gly Glu Asn Ala Ser Gly Lys
        795   800   805

tac tgt ggg aaa acc caa acc atc ttt ctg aag tat cca cag gag aaa   2560
Tyr Cys Gly Lys Thr Gln Thr Ile Phe Leu Lys Tyr Pro Gln Glu Lys
    810   815   820

aac aac ggg cca aag gtg cct gtg gag ttg cga gtg aac atc tgg cta   2608
Asn Asn Gly Pro Lys Val Pro Val Glu Leu Arg Val Asn Ile Trp Leu
825   830   835   840

ggc tta agt gct gtg gag aag aag ttt aac agc ttc gca gaa gga act   2656
Gly Leu Ser Ala Val Glu Lys Lys Phe Asn Ser Phe Ala Glu Gly Thr
              845   850   855

ttc acc gtc ttt gct gaa atg tat gaa aat caa gct ctc atg ttt gga   2704
Phe Thr Val Phe Ala Glu Met Tyr Glu Asn Gln Ala Leu Met Phe Gly
              860   865   870

aaa tgg ggt act tct gga tta gta gga cgt cat aag ttt tct gat gtc   2752
Lys Trp Gly Thr Ser Gly Leu Val Gly Arg His Lys Phe Ser Asp Val
              875   880   885

aca gga aaa ata aaa ctc aag agg gaa ttt ttt ctg cct cca aaa ggc   2800
Thr Gly Lys Ile Lys Leu Lys Arg Glu Phe Phe Leu Pro Pro Lys Gly
        890   895   900

tgg gaa tgg gaa gga gag tgg ata gtt gat cct gaa aga agc ttg ctg   2848
Trp Glu Trp Glu Gly Glu Trp Ile Val Asp Pro Glu Arg Ser Leu Leu
905   910   915   920

act gag gca gat gca ggt cac acg gag ttc act gat gaa gtc tat cag   2896
Thr Glu Ala Asp Ala Gly His Thr Glu Phe Thr Asp Glu Val Tyr Gln
              925   930   935

aac gag agc cgc tac ccc ggg ggc gac tgg aag ccg gcc gag gac acc   2944
Asn Glu Ser Arg Tyr Pro Gly Gly Asp Trp Lys Pro Ala Glu Asp Thr
        940   945   950

tac acg gat gcg aac ggc gat aaa gca gca tca ccc agc gag ttg act   2992
Tyr Thr Asp Ala Asn Gly Asp Lys Ala Ala Ser Pro Ser Glu Leu Thr
        955   960   965

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tgt cct cca ggt tgg gaa tgg gaa gat gat gca tgg tct tat gac ata      3040
Cys Pro Pro Gly Trp Glu Trp Glu Asp Asp Ala Trp Ser Tyr Asp Ile
    970             975                 980

aat cga gcg gtg gat gag aaa ggc tgg gaa tat gga atc acc att cct      3088
Asn Arg Ala Val Asp Glu Lys Gly Trp Glu Tyr Gly Ile Thr Ile Pro
985             990                 995                 1000

cct gat cat aag ccc aaa tcc tgg gtt gca gca gag aaa atg tac         3133
Pro Asp His Lys Pro Lys Ser Trp Val Ala Ala Glu Lys Met Tyr
                1005            1010            1015

cac act cat aga cgg cga agg ctg gtc cga aaa cgc aag aaa gat         3178
His Thr His Arg Arg Arg Arg Leu Val Arg Lys Arg Lys Lys Asp
                1020            1025            1030

tta aca cag act gct tca agc acc gca agg gcc atg gag gaa ttg         3223
Leu Thr Gln Thr Ala Ser Ser Thr Ala Arg Ala Met Glu Glu Leu
                1035            1040            1045

caa gac caa gag ggc tgg gaa tat gct tct cta att ggc tgg aaa         3268
Gln Asp Gln Glu Gly Trp Glu Tyr Ala Ser Leu Ile Gly Trp Lys
                1050            1055            1060

ttt cac tgg aaa caa cgt agt tca gat acc ttc cgc cgc aga cgc         3313
Phe His Trp Lys Gln Arg Ser Ser Asp Thr Phe Arg Arg Arg Arg
                1065            1070            1075

tgg agg aga aaa atg gct cct tca gaa aca cat ggt gca gct gcc         3358
Trp Arg Arg Lys Met Ala Pro Ser Glu Thr His Gly Ala Ala Ala
                1080            1085            1090

atc ttt aaa ctt gaa ggt gcc ctt ggg gca gac act acc gaa gat         3403
Ile Phe Lys Leu Glu Gly Ala Leu Gly Ala Asp Thr Thr Glu Asp
                1095            1100            1105

ggg gat gag aag agc ctg gag aaa cag aag cac agt gcc acc act         3448
Gly Asp Glu Lys Ser Leu Glu Lys Gln Lys His Ser Ala Thr Thr
                1110            1115            1120

gtg ttc gga gca aac acc ccc att gtt tcc tgc aat ttt gac aga         3493
Val Phe Gly Ala Asn Thr Pro Ile Val Ser Cys Asn Phe Asp Arg
                1125            1130            1135

gtc tac atc tac cat ctg cgc tgc tat gtc tat caa gcc aga aac         3538
Val Tyr Ile Tyr His Leu Arg Cys Tyr Val Tyr Gln Ala Arg Asn
                1140            1145            1150

ctc ttg gct tta gat aag gat agc ttt tca gat cca tat gct cat         3583
Leu Leu Ala Leu Asp Lys Asp Ser Phe Ser Asp Pro Tyr Ala His
                1155            1160            1165

atc tgt ttc ctc cat cgg agc aaa acc act gag atc atc cat tca         3628
Ile Cys Phe Leu His Arg Ser Lys Thr Thr Glu Ile Ile His Ser
                1170            1175            1180

acc ctg aat ccc acg tgg gac caa aca att ata ttc gat gaa gtt         3673
Thr Leu Asn Pro Thr Trp Asp Gln Thr Ile Ile Phe Asp Glu Val
                1185            1190            1195

gaa atc tat ggg gaa ccc caa aca gtt cta cag aat cca ccc aaa         3718
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Glu Ile Tyr Gly Glu  Pro Gln Thr Val Leu  Gln Asn Pro Pro Lys
        1200              1205              1210

gtt atc atg gaa ctt  ttt gac aat gac caa  gtg ggc aaa gat gaa    3763
Val Ile Met Glu Leu  Phe Asp Asn Asp Gln  Val Gly Lys Asp Glu
        1215              1220              1225

ttt tta gga cga agc  att ttc tct cct gtg  gtg aaa ctg aac tca    3808
Phe Leu Gly Arg Ser  Ile Phe Ser Pro Val  Val Lys Leu Asn Ser
        1230              1235              1240

gaa atg gac atc aca  ccc aaa ctt ctc tgg  cac cca gta atg aat    3853
Glu Met Asp Ile Thr  Pro Lys Leu Leu Trp  His Pro Val Met Asn
        1245              1250              1255

gga gac aaa gcc tgc  ggg gat gtt ctt gta  act gca gag ctg att    3898
Gly Asp Lys Ala Cys  Gly Asp Val Leu Val  Thr Ala Glu Leu Ile
        1260              1265              1270

ctg agg ggc aag gat  ggc tcc aac ctt ccc  att ctt ccc cct caa    3943
Leu Arg Gly Lys Asp  Gly Ser Asn Leu Pro  Ile Leu Pro Pro Gln
        1275              1280              1285

agg gcg cca aat cta  tac atg gtc ccc cag  ggg atc agg cct gtg    3988
Arg Ala Pro Asn Leu  Tyr Met Val Pro Gln  Gly Ile Arg Pro Val
        1290              1295              1300

gtc cag ctc act gcc  att gag att cta gct  tgg ggc tta aga aat    4033
Val Gln Leu Thr Ala  Ile Glu Ile Leu Ala  Trp Gly Leu Arg Asn
        1305              1310              1315

atg aaa aac ttc cag  atg gct tct atc aca  tcc ccc agt ctt gtt    4078
Met Lys Asn Phe Gln  Met Ala Ser Ile Thr  Ser Pro Ser Leu Val
        1320              1325              1330

gtg gag tgt gga gga  gaa agg gtg gaa tcg  gtg gtg atc aaa aac    4123
Val Glu Cys Gly Gly  Glu Arg Val Glu Ser  Val Val Ile Lys Asn
        1335              1340              1345

ctt aag aag aca ccc  aac ttt cca agt tct  gtt ctc ttc atg aaa    4168
Leu Lys Lys Thr Pro  Asn Phe Pro Ser Ser  Val Leu Phe Met Lys
        1350              1355              1360

gtg ttc ttg ccc aag  gag gaa ttg tac atg  ccc cca ctg gtg atc    4213
Val Phe Leu Pro Lys  Glu Glu Leu Tyr Met  Pro Pro Leu Val Ile
        1365              1370              1375

aag gtc atc gac cac  agg cag ttt ggg cgg  aag cct gtc gtc ggc    4258
Lys Val Ile Asp His  Arg Gln Phe Gly Arg  Lys Pro Val Val Gly
        1380              1385              1390

cag tgc acc atc gag  cgc ctg gac cgc ttt  cgc tgt gac cct tat    4303
Gln Cys Thr Ile Glu  Arg Leu Asp Arg Phe  Arg Cys Asp Pro Tyr
        1395              1400              1405

gca ggg aaa gag gac  atc gtc cca cag ctc  aaa gcc tcc ctt ctg    4348
Ala Gly Lys Glu Asp  Ile Val Pro Gln Leu  Lys Ala Ser Leu Leu
        1410              1415              1420

tct gcc cca cca tgc  cgg gac atc gtt atc  gaa atg gaa gac acc    4393
Ser Ala Pro Pro Cys  Arg Asp Ile Val Ile  Glu Met Glu Asp Thr
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166

<pre>
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aaa cca tta ctg gct   tct aag ctg aca gaa   aag gag gaa gaa atc   4438
Lys Pro Leu Leu Ala   Ser Lys Leu Thr Glu   Lys Glu Glu Glu Ile
             1440   1445   1450

gtg gac tgg tgg agt   aaa ttt tat gct tcc   tca ggg gaa cat gaa   4483
Val Asp Trp Trp Ser   Lys Phe Tyr Ala Ser   Ser Gly Glu His Glu
             1455   1460   1465

aaa tgc gga cag tat   att cag aaa ggc tat   tcc aag ctc aag ata   4528
Lys Cys Gly Gln Tyr   Ile Gln Lys Gly Tyr   Ser Lys Leu Lys Ile
             1470   1475   1480

tat aat tgt gaa cta   gaa aat gta gca gaa   ttt gag ggc ctg aca   4573
Tyr Asn Cys Glu Leu   Glu Asn Val Ala Glu   Phe Glu Gly Leu Thr
             1485   1490   1495

gac ttc tca gat acg   ttc aag ttg tac cga   ggc aag tcg gat gaa   4618
Asp Phe Ser Asp Thr   Phe Lys Leu Tyr Arg   Gly Lys Ser Asp Glu
             1500   1505   1510

aat gaa gat cct tct   gtg gtt gga gag ttt   aag ggc tcc ttt cgg   4663
Asn Glu Asp Pro Ser   Val Val Gly Glu Phe   Lys Gly Ser Phe Arg
             1515   1520   1525

atc tac cct ctg ccg   gat gac ccc agc gtg   cca gcc cct ccc aga   4708
Ile Tyr Pro Leu Pro   Asp Asp Pro Ser Val   Pro Ala Pro Pro Arg
             1530   1535   1540

cag ttt cgg gaa tta   cct gac agc gtc cca   cag gaa tgc acg gtt   4753
Gln Phe Arg Glu Leu   Pro Asp Ser Val Pro   Gln Glu Cys Thr Val
             1545   1550   1555

agg att tac att gtt   cga ggc tta gag ctc   cag ccc cag gac aac   4798
Arg Ile Tyr Ile Val   Arg Gly Leu Glu Leu   Gln Pro Gln Asp Asn
             1560   1565   1570

aat ggc ctg tgt gac   cct tac ata aaa ata   aca ctg ggc aaa aaa   4843
Asn Gly Leu Cys Asp   Pro Tyr Ile Lys Ile   Thr Leu Gly Lys Lys
             1575   1580   1585

gtc att gaa gac cga   gat cac tac att ccc   aac act ctc aac cca   4888
Val Ile Glu Asp Arg   Asp His Tyr Ile Pro   Asn Thr Leu Asn Pro
             1590   1595   1600

gtc ttt ggc agg atg   tac gaa ctg agc tgc   tac tta cct caa gaa   4933
Val Phe Gly Arg Met   Tyr Glu Leu Ser Cys   Tyr Leu Pro Gln Glu
             1605   1610   1615

aaa gac ctg aaa att   tct gtc tat gat tat   gac acc ttt acc cgg   4978
Lys Asp Leu Lys Ile   Ser Val Tyr Asp Tyr   Asp Thr Phe Thr Arg
             1620   1625   1630

gat gaa aaa gta gga   gaa aca att att gat   ctg gaa aac cga ttc   5023
Asp Glu Lys Val Gly   Glu Thr Ile Ile Asp   Leu Glu Asn Arg Phe
             1635   1640   1645

ctt tcc cgc ttt ggg   tcc cac tgc ggc ata   cca gag gag tac tgt   5068
Leu Ser Arg Phe Gly   Ser His Cys Gly Ile   Pro Glu Glu Tyr Cys
             1650   1655   1660
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167

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gtt tct gga gtc aat   acc tgg cga gat caa   ctg aga cca aca cag      5113
Val Ser Gly Val Asn   Thr Trp Arg Asp Gln   Leu Arg Pro Thr Gln
            1665                 1670                    1675


ctg ctt caa aat gtc   gcc aga ttc aaa ggc   ttc cca caa ccc atc      5158
Leu Leu Gln Asn Val   Ala Arg Phe Lys Gly   Phe Pro Gln Pro Ile
            1680                 1685                    1690


ctt tcc gaa gat ggg   agt aga atc aga tat   gga gga cga gac tac      5203
Leu Ser Glu Asp Gly   Ser Arg Ile Arg Tyr   Gly Gly Arg Asp Tyr
            1695                 1700                    1705


agc ttg gat gaa ttt   gaa gcc aac aaa atc   ctg cac cag cac ctc      5248
Ser Leu Asp Glu Phe   Glu Ala Asn Lys Ile   Leu His Gln His Leu
            1710                 1715                    1720


ggg gcc cct gaa gag   cgg ctt gct ctt cac   atc ctc agg act cag      5293
Gly Ala Pro Glu Glu   Arg Leu Ala Leu His   Ile Leu Arg Thr Gln
            1725                 1730                    1735


ggg ctg gtc cct gag   cac gtg gaa aca agg   act ttg cac agc acc      5338
Gly Leu Val Pro Glu   His Val Glu Thr Arg   Thr Leu His Ser Thr
            1740                 1745                    1750


ttc cag ccc aac att   tcc cag gga aaa ctt   cag atg tgg gtg gat      5383
Phe Gln Pro Asn Ile   Ser Gln Gly Lys Leu   Gln Met Trp Val Asp
            1755                 1760                    1765


gtt ttc ccc aag agt   ttg ggg cca cca ggc   cct cct ttc aac atc      5428
Val Phe Pro Lys Ser   Leu Gly Pro Pro Gly   Pro Pro Phe Asn Ile
            1770                 1775                    1780


aca ccc cgg aaa gcc   aag aaa tac tac ctg   cgt gtg atc atc tgg      5473
Thr Pro Arg Lys Ala   Lys Lys Tyr Tyr Leu   Arg Val Ile Ile Trp
            1785                 1790                    1795


aac acc aag gac gtt   atc ttg gac gag aaa   agc atc aca gga gag      5518
Asn Thr Lys Asp Val   Ile Leu Asp Glu Lys   Ser Ile Thr Gly Glu
            1800                 1805                    1810


gaa atg agt gac atc   tac gtc aaa ggc tgg   att cct ggc aat gaa      5563
Glu Met Ser Asp Ile   Tyr Val Lys Gly Trp   Ile Pro Gly Asn Glu
            1815                 1820                    1825


gaa aac aaa cag aaa   aca gat gtc cat tac   aga tct ttg gat ggt      5608
Glu Asn Lys Gln Lys   Thr Asp Val His Tyr   Arg Ser Leu Asp Gly
            1830                 1835                    1840


gaa ggg aat ttt aac   tgg cga ttt gtt ttc   ccg ttt gac tac ctt      5653
Glu Gly Asn Phe Asn   Trp Arg Phe Val Phe   Pro Phe Asp Tyr Leu
            1845                 1850                    1855


cca gcc gaa caa ctc   tgt atc gtt gcg aaa   aaa gag cat ttc tgg      5698
Pro Ala Glu Gln Leu   Cys Ile Val Ala Lys   Lys Glu His Phe Trp
            1860                 1865                    1870


agt att gac caa acg   gaa ttt cga atc cca   ccc agg ctg atc att      5743
Ser Ile Asp Gln Thr   Glu Phe Arg Ile Pro   Pro Arg Leu Ile Ile
            1875                 1880                    1885
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  cag ata tgg gac aat   gac aag ttt tct ctg   gat gac tac ttg ggt      5788
  Gln Ile Trp Asp Asn   Asp Lys Phe Ser Leu   Asp Asp Tyr Leu Gly
              1890                 1895                      1900

  ttc cta gaa ctt gac   ttg cgt cac acg atc   att cct gca aaa tca      5833
  Phe Leu Glu Leu Asp   Leu Arg His Thr Ile   Ile Pro Ala Lys Ser
              1905                 1910                      1915

  cca gag aaa tgc agg   ttg gac atg att ccg   gac ctc aaa gcc atg      5878
  Pro Glu Lys Cys Arg   Leu Asp Met Ile Pro   Asp Leu Lys Ala Met
              1920                 1925                      1930

  aac ccc ctt aaa gcc   aag aca gcc tcc ctc   ttt gag cag aag tcc      5923
  Asn Pro Leu Lys Ala   Lys Thr Ala Ser Leu   Phe Glu Gln Lys Ser
              1935                 1940                      1945

  atg aaa gga tgg tgg   cca tgc tac gca gag   aaa gat ggc gcc cgc      5968
  Met Lys Gly Trp Trp   Pro Cys Tyr Ala Glu   Lys Asp Gly Ala Arg
              1950                 1955                      1960

  gta atg gct ggg aaa   gtg gag atg aca ttg   gaa atc ctc aac gag      6013
  Val Met Ala Gly Lys   Val Glu Met Thr Leu   Glu Ile Leu Asn Glu
              1965                 1970                      1975

  aag gag gcc gac gag   agg cca gcc ggg aag   ggg cgg gac gaa ccc      6058
  Lys Glu Ala Asp Glu   Arg Pro Ala Gly Lys   Gly Arg Asp Glu Pro
              1980                 1985                      1990

  aac atg aac ccc aag   ctg gac tta cca aat   cga cca gaa acc tcc      6103
  Asn Met Asn Pro Lys   Leu Asp Leu Pro Asn   Arg Pro Glu Thr Ser
              1995                 2000                      2005

  ttc ctc tgg ttc acc   aac cca tgc aag acc   atg aag ttc atc gtg      6148
  Phe Leu Trp Phe Thr   Asn Pro Cys Lys Thr   Met Lys Phe Ile Val
              2010                 2015                      2020

  tgg cgc cgc ttt aag   tgg gtc atc atc ggc   ttg ctg ttc ctg ctt      6193
  Trp Arg Arg Phe Lys   Trp Val Ile Ile Gly   Leu Leu Phe Leu Leu
              2025                 2030                      2035

  atc ctg ctg ctc ttc   gtg gcc gtg ctc ctc   tac tct ttg ccg aac      6238
  Ile Leu Leu Leu Phe   Val Ala Val Leu Leu   Tyr Ser Leu Pro Asn
              2040                 2045                      2050

  tat ttg tca atg aag   att gta aag cca aat   gtg taa caaaggcaaa       6284
  Tyr Leu Ser Met Lys   Ile Val Lys Pro Asn   Val
              2055                 2060
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  ggcttcattt caagagtcat ccagcaatga gagaatcctg cctctgtaga ccaacatcca    6344      -.

  gtgtgatttt gtgtctgaga ccacacccca gtagcaggtt acgccatgtc accgagcccc    6404

  attgattccc agagggtctt agtcctggaa agtcaggcca acaagcaacg tttgcatcat    6464

  gttatctctt aagtattaaa agttttattt tctaaagttt aaatcatgtt tttcaaaata    6524

  ttttttcaagg tggctggttc catttaaaaa tcatcttttt atatgtgtct tcggttctag   6584

  acttcagctt ttggaaattg ctaaatagaa ttcaaaaatc tctgcatcct gaggtgatat    6644      -..

  acttcatatt tgtaatcaac tgaaagagct gtgcattata aaatcagtta gaatagttag    6704
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aacaattctt atttatgccc acaaccattg ctatattttg tatggatgtc ataaaagtct   6764

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aaaaa   6829

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Phe Gly Lys Pro Asp Pro Ile Val Ser Val Ile Phe Lys Asp Glu Lys
            20   25   30

Lys Lys Thr Lys Lys Val Asp Asn Glu Leu Asn Pro Val Trp Asn Glu
            35   40   45

Ile Leu Glu Phe Asp Leu Arg Gly Ile Pro Leu Asp Phe Ser Ser Ser
        50   55   60

Leu Gly Ile Ile Val Lys Asp Phe Glu Thr Ile Gly Gln Asn Lys Leu
65   70   75   80

Ile Gly Thr Ala Thr Val Ala Leu Lys Asp Leu Thr Gly Asp Gln Ser
                85   90   95

Arg Ser Leu Pro Tyr Lys Leu Ile Ser Leu Leu Asn Glu Lys Gly Gln
            100   105   110

Asp Thr Gly Ala Thr Ile Asp Leu Val Ile Gly Tyr Asp Pro Pro Ser
            115   120   125

Ala Pro His Pro Asn Asp Leu Ser Gly Pro Ser Val Pro Gly Met Gly
            130   135   140

Gly Asp Gly Glu Glu Asp Glu Gly Asp Glu Asp Arg Leu Asp Asn Ala
145   150   155   160

Val Arg Gly Pro Gly Pro Lys Gly Pro Val Gly Thr Val Ser Glu Ala
                165   170   175

Gln Leu Ala Arg Arg Leu Thr Lys Val Lys Asn Ser Arg Arg Met Leu
            180   185   190

Ser Asn Lys Pro Gln Asp Phe Gln Ile Arg Val Arg Val Ile Glu Gly
    195   200   205

Arg Gln Leu Ser Gly Asn Asn Ile Arg Pro Val Val Lys Val His Val
    210   215   220

Cys Gly Gln Thr His Arg Thr Arg Ile Lys Arg Gly Asn Asn Pro Phe
225   230   235   240

Phe Asp Glu Leu Phe Phe Tyr Asn Val Asn Met Thr Pro Ser Glu Leu
        245   250   255

Met Asp Glu Ile Ile Ser Ile Arg Val Tyr Asn Ser His Ser Leu Arg
      260   265   270

Ala Asp Cys Leu Met Gly Glu Phe Lys Ile Asp Val Gly Phe Val Tyr
      275   280   285

Asp Glu Pro Gly His Ala Val Met Arg Lys Trp Leu Leu Leu Asn Asp
    290   295   300

Pro Glu Asp Thr Ser Ser Gly Ser Lys Gly Tyr Met Lys Val Ser Met
305   310   315   320

Phe Val Leu Gly Thr Gly Asp Glu Pro Pro Pro Glu Arg Arg Asp Arg
        325   330   335

Asp Asn Asp Ser Asp Asp Val Glu Ser Asn Leu Leu Leu Pro Ala Gly
        340   345   350

Ile Ala Leu Arg Trp Val Thr Phe Leu Leu Lys Ile Tyr Arg Ala Glu
      355   360   365

Asp Ile Pro Gln Met Asp Asp Ala Phe Ser Gln Thr Val Lys Glu Ile
    370   375   380

Phe Gly Gly Asn Ala Asp Lys Lys Asn Leu Val Asp Pro Phe Val Glu

Val Ser Phe Ala Gly Lys Lys Val Cys Thr Asn Ile Ile Glu Lys Asn
        405   410   415

Ala Asn Pro Glu Trp Asn Gln Val Val Asn Leu Gln Ile Lys Phe Pro
    420   425   430

Ser Val Cys Glu Lys Ile Lys Leu Thr Ile Tyr Asp Trp Asp Arg Leu
        435   440   445

Thr Lys Asn Asp Val Val Gly Thr Thr Tyr Leu His Leu Ser Lys Ile
    450   455   460

Ala Ala Ser Gly Gly Glu Val Glu Asp Phe Ser Ser Ser Gly Thr Gly
465   470   475   480

Ala Ala Ser Tyr Thr Val Asn Thr Gly Glu Thr Glu Val Gly Phe Val
            485   490   495

Pro Thr Phe Gly Pro Cys Tyr Leu Asn Leu Tyr Gly Ser Pro Arg Glu
        500   505   510

Tyr Thr Gly Phe Pro Asp Pro Tyr Asp Glu Leu Asn Thr Gly Lys Gly
    515   520   525

Glu Gly Val Ala Tyr Arg Gly Arg Ile Leu Val Glu Leu Ala Thr Phe
    530   535   540

Leu Glu Lys Thr Pro Pro Asp Lys Lys Leu Glu Pro Ile Ser Asn Asp
545   550   555   560

Asp Leu Leu Val Val Glu Lys Tyr Gln Arg Arg Arg Lys Tyr Ser Leu
            565   570   575

Ser Ala Val Phe His Ser Ala Thr Met Leu Gln Asp Val Gly Glu Ala
        580   585   590

Ile Gln Phe Glu Val Ser Ile Gly Asn Tyr Gly Asn Lys Phe Asp Thr
    595   600   605

Thr Cys Lys Pro Leu Ala Ser Thr Thr Gln Tyr Ser Arg Ala Val Phe
    610   615   620

Asp Gly Asn Tyr Tyr Tyr Tyr Leu Pro Trp Ala His Thr Lys Pro Val
625   630   635   640

Val Thr Leu Thr Ser Tyr Trp Glu Asp Ile Ser His Arg Leu Asp Ala
            645   650   655

Val Asn Thr Leu Leu Ala Met Ala Glu Arg Leu Gln Thr Asn Ile Glu
            660   665   670

Ala Leu Lys Ser Gly Ile Gln Gly Lys Ile Pro Ala Asn Gln Leu Ala

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              675                   680                  685

Glu Leu Trp Leu Lys Leu Ile Asp Glu Val Ile Glu Asp Thr Arg Tyr
        690                   695                  700

Thr Leu Pro Leu Thr Glu Gly Lys Ala Asn Val Thr Val Leu Asp Thr
705                   710                  715                  720

Gln Ile Arg Lys Leu Arg Ser Arg Ser Leu Ser Gln Ile His Glu Ala
                725                   730                  735

Ala Val Arg Met Arg Ser Glu Ala Thr Asp Val Lys Ser Thr Leu Ala
              740                   745                  750

Glu Ile Glu Asp Trp Leu Asp Lys Leu Met Gln Leu Thr Glu Glu Pro
          755                   760                  765

Gln Asn Ser Met Pro Asp Ile Ile Ile Trp Met Ile Arg Gly Glu Lys
    770                   775                  780

Arg Leu Ala Tyr Ala Arg Ile Pro Ala His Gln Val Leu Tyr Ser Thr
785                   790                  795                  800

Ser Gly Glu Asn Ala Ser Gly Lys Tyr Cys Gly Lys Thr Gln Thr Ile
              805                   810                  815

Phe Leu Lys Tyr Pro Gln Glu Lys Asn Asn Gly Pro Lys Val Pro Val
          820                   825                  830

Glu Leu Arg Val Asn Ile Trp Leu Gly Leu Ser Ala Val Glu Lys Lys
          835                   840                  845

Phe Asn Ser Phe Ala Glu Gly Thr Phe Thr Val Phe Ala Glu Met Tyr
    850                   855                  860

Glu Asn Gln Ala Leu Met Phe Gly Lys Trp Gly Thr Ser Gly Leu Val
865                   870                  875                  880

Gly Arg His Lys Phe Ser Asp Val Thr Gly Lys Ile Lys Leu Lys Arg
              885                   890                  895

Glu Phe Phe Leu Pro Pro Lys Gly Trp Glu Trp Glu Gly Glu Trp Ile

Val Asp Pro Glu Arg Ser Leu Leu Thr Glu Ala Asp Ala Gly His Thr
    915                   920                  925
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Glu Phe Thr Asp Glu Val Tyr Gln Asn Glu Ser Arg Tyr Pro Gly Gly
    930   935   940

Asp Trp Lys Pro Ala Glu Asp Thr Tyr Thr Asp Ala Asn Gly Asp Lys
945   950   955   960

Ala Ala Ser Pro Ser Glu Leu Thr Cys Pro Pro Gly Trp Glu Trp Glu
                965   970   975

Asp Asp Ala Trp Ser Tyr Asp Ile Asn Arg Ala Val Asp Glu Lys Gly
            980   985   990

Trp Glu Tyr Gly Ile Thr Ile Pro Pro Asp His Lys Pro Lys Ser Trp
        995   1000   1005

Val Ala Ala Glu Lys Met Tyr His Thr His Arg Arg Arg Arg Leu
    1010   1015   1020

Val Arg Lys Arg Lys Lys Asp Leu Thr Gln Thr Ala Ser Ser Thr
    1025   1030   1035

Ala Arg Ala Met Glu Glu Leu Gln Asp Gln Glu Gly Trp Glu Tyr
    1040   1045   1050

Ala Ser Leu Ile Gly Trp Lys Phe His Trp Lys Gln Arg Ser Ser
    1055   1060   1065

Asp Thr Phe Arg Arg Arg Arg Trp Arg Arg Lys Met Ala Pro Ser
    1070   1075   1080

Glu Thr His Gly Ala Ala Ala Ile Phe Lys Leu Glu Gly Ala Leu
    1085   1090   1095

Gly Ala Asp Thr Thr Glu Asp Gly Asp Glu Lys Ser Leu Glu Lys
    1100   1105   1110

Gln Lys His Ser Ala Thr Thr Val Phe Gly Ala Asn Thr Pro Ile
    1115   1120   1125

Val Ser Cys Asn Phe Asp Arg Val Tyr Ile Tyr His Leu Arg Cys
    1130   1135   1140

Tyr Val Tyr Gln Ala Arg Asn Leu Leu Ala Leu Asp Lys Asp Ser
    1145   1150   1155

Phe Ser Asp Pro Tyr Ala His Ile Cys Phe Leu His Arg Ser Lys
     1160   1165   1170

Thr Thr Glu Ile Ile His Ser Thr Leu Asn Pro Thr Trp Asp Gln
     1175   1180   1185

Thr Ile Ile Phe Asp Glu Val Glu Ile Tyr Gly Glu Pro Gln Thr
     1190   1195   1200

Val Leu Gln Asn Pro Pro Lys Val Ile Met Glu Leu Phe Asp Asn
     1205   1210   1215

Asp Gln Val Gly Lys Asp Glu Phe Leu Gly Arg Ser Ile Phe Ser
     1220   1225   1230

Pro Val Val Lys Leu Asn Ser Glu Met Asp Ile Thr Pro Lys Leu
     1235   1240   1245

Leu Trp His Pro Val Met Asn Gly Asp Lys Ala Cys Gly Asp Val
     1250   1255   1260

Leu Val Thr Ala Glu Leu Ile Leu Arg Gly Lys Asp Gly Ser Asn
     1265   1270   1275

Leu Pro Ile Leu Pro Pro Gln Arg Ala Pro Asn Leu Tyr Met Val
     1280   1285   1290

Pro Gln Gly Ile Arg Pro Val Val Gln Leu Thr Ala Ile Glu Ile
     1295   1300   1305

Leu Ala Trp Gly Leu Arg Asn Met Lys Asn Phe Gln Met Ala Ser
     1310   1315   1320

Ile Thr Ser Pro Ser Leu Val Val Glu Cys Gly Gly Glu Arg Val
     1325   1330   1335

Glu Ser Val Val Ile Lys Asn Leu Lys Lys Thr Pro Asn Phe Pro
     1340   1345   1350

Ser Ser Val Leu Phe Met Lys Val Phe Leu Pro Lys Glu Glu Leu
     1355   1360   1365

Tyr Met Pro Pro Leu Val Ile Lys Val Ile Asp His Arg Gln Phe
     1370   1375   1380

Gly Arg Lys Pro Val Val Gly Gln Cys Thr Ile Glu Arg Leu Asp

1385   1390   1395

Arg Phe Arg Cys Asp Pro Tyr Ala Gly Lys Glu Asp Ile Val Pro
    1400   1405   1410

Gln Leu Lys Ala Ser Leu Leu Ser Ala Pro Pro Cys Arg Asp Ile
    1415   1420   1425

Val Ile Glu Met Glu Asp Thr Lys Pro Leu Leu Ala Ser Lys Leu
    1430   1435   1440

Thr Glu Lys Glu Glu Glu Ile Val Asp Trp Trp Ser Lys Phe Tyr
    1445   1450   1455

Ala Ser Ser Gly Glu His Glu Lys Cys Gly Gln Tyr Ile Gln Lys
    1460   1465   1470

Gly Tyr Ser Lys Leu Lys Ile Tyr Asn Cys Glu Leu Glu Asn Val
    1475   1480   1485

Ala Glu Phe Glu Gly Leu Thr Asp Phe Ser Asp Thr Phe Lys Leu
    1490   1495   1500

Tyr Arg Gly Lys Ser Asp Glu Asn Glu Asp Pro Ser Val Val Gly

Glu Phe Lys Gly Ser Phe Arg Ile Tyr Pro Leu Pro Asp Asp Pro
    1520   1525   1530

Ser Val Pro Ala Pro Pro Arg Gln Phe Arg Glu Leu Pro Asp Ser
    1535   1540   1545

Val Pro Gln Glu Cys Thr Val Arg Ile Tyr Ile Val Arg Gly Leu
    1550   1555   1560

Glu Leu Gln Pro Gln Asp Asn Asn Gly Leu Cys Asp Pro Tyr Ile
    1565   1570   1575

Lys Ile Thr Leu Gly Lys Lys Val Ile Glu Asp Arg Asp His Tyr
    1580   1585   1590

Ile Pro Asn Thr Leu Asn Pro Val Phe Gly Arg Met Tyr Glu Leu
    1595   1600   1605

Ser Cys Tyr Leu Pro Gln Glu Lys Asp Leu Lys Ile Ser Val Tyr
    1610   1615   1620

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Asp Tyr  Asp Thr Phe Thr Arg  Asp Glu Lys Val Gly  Glu Thr Ile
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Ile Asp  Leu Glu Asn Arg Phe  Leu Ser Arg Phe Gly  Ser His Cys
    1640                1645              1650


Gly Ile  Pro Glu Glu Tyr Cys  Val Ser Gly Val Asn  Thr Trp Arg
    1655                1660              1665


Asp Gln  Leu Arg Pro Thr Gln  Leu Leu Gln Asn Val  Ala Arg Phe
    1670                1675              1680


Lys Gly  Phe Pro Gln Pro Ile  Leu Ser Glu Asp Gly  Ser Arg Ile
    1685                1690              1695


Arg Tyr  Gly Gly Arg Asp Tyr  Ser Leu Asp Glu Phe  Glu Ala Asn
    1700                1705              1710


Lys Ile  Leu His Gln His Leu  Gly Ala Pro Glu Glu  Arg Leu Ala
    1715                1720              1725


Leu His  Ile Leu Arg Thr Gln  Gly Leu Val Pro Glu  His Val Glu
    1730                1735               1740


Thr Arg  Thr Leu His Ser Thr  Phe Gln Pro Asn Ile  Ser Gln Gly
    1745                1750              1755


Lys Leu  Gln Met Trp Val Asp  Val Phe Pro Lys Ser  Leu Gly Pro
    1760                1765              1770


Pro Gly  Pro Pro Phe Asn Ile  Thr Pro Arg Lys Ala  Lys Lys Tyr
    1775                1780              1785


Tyr Leu  Arg Val Ile Ile Trp  Asn Thr Lys Asp Val  Ile Leu Asp
    1790                1795              1800


Glu Lys  Ser Ile Thr Gly Glu  Glu Met Ser Asp Ile  Tyr Val Lys
    1805                1810              1815


Gly Trp  Ile Pro Gly Asn Glu  Glu Asn Lys Gln Lys  Thr Asp Val
    1820                1825              1830


His Tyr  Arg Ser Leu Asp Gly  Glu Gly Asn Phe Asn  Trp Arg Phe
    1835                1840              1845


Val Phe  Pro Phe Asp Tyr Leu  Pro Ala Glu Gln Leu  Cys Ile Val
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177

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              1850              1855              1860


Ala Lys  Lys Glu His Phe Trp  Ser Ile Asp Gln Thr  Glu Phe Arg
    1865              1870              1875


Ile Pro  Pro Arg Leu Ile Ile  Gln Ile Trp Asp Asn  Asp Lys Phe
    1880              1885              1890


Ser Leu  Asp Asp Tyr Leu Gly  Phe Leu Glu Leu Asp  Leu Arg His
    1895              1900              1905


Thr Ile  Ile Pro Ala Lys Ser  Pro Glu Lys Cys Arg  Leu Asp Met
    1910              1915              1920


Ile Pro  Asp Leu Lys Ala Met  Asn Pro Leu Lys Ala  Lys Thr Ala
    1925              1930              1935


Ser Leu  Phe Glu Gln Lys Ser  Met Lys Gly Trp Trp  Pro Cys Tyr
    1940              1945              1950


Ala Glu  Lys Asp Gly Ala Arg  Val Met Ala Gly Lys  Val Glu Met
    1955              1960              1965


Thr Leu  Glu Ile Leu Asn Glu  Lys Glu Ala Asp Glu  Arg Pro Ala
    1970              1975              1980


Gly Lys  Gly Arg Asp Glu Pro  Asn Met Asn Pro Lys  Leu Asp Leu
    1985              1990              1995


Pro Asn  Arg Pro Glu Thr Ser  Phe Leu Trp Phe Thr  Asn Pro Cys
    2000              2005              2010


Lys Thr  Met Lys Phe Ile Val  Trp Arg Arg Phe Lys  Trp Val Ile
    2015              2020              2025


Ile Gly  Leu Leu Phe Leu Leu  Ile Leu Leu Leu Phe  Val Ala Val
    2030              2035              2040


Leu Leu  Tyr Ser Leu Pro Asn  Tyr Leu Ser Met Lys  Ile Val Lys
    2045              2050              2055


Pro Asn  Val
    2060


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